

Genes version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:45:34 ; Search time 13266.4 Seconds  
(without alignments)  
11198.460 Million cell updates/sec

Title: US-09-719-485-1  
Perfect score: 3066  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_to.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3066	100.0	3066	6	BD211242 Cloning a
2	3050.8	99.5	163284	9	AL137000 Human DNA
3	3050.8	99.5	341560	2	AL596304 Homo sapi
4	3050.8	99.5	349980	6	AX711879 Sequence
5	3050.8	99.5	349980	6	AX739961 Sequence
6	2026	66.1	2040	9	AF034632 Homo sapi
7	1038	33.9	1161	6	AX154591 Sequence
8	1038	33.9	1390	6	BD211244 Cloning a
9	901	29.4	1239	6	BD211243 Cloning a
10	901	29.4	1239	6	CQ724376 Sequence
11	901	29.4	1239	6	CQ831648 Sequence
12	901	29.4	1239	6	AX154589 Sequence
13	901	29.4	1239	6	AX549187 Sequence
14	901	29.4	1239	6	AX572965 Sequence
15	901	29.4	1239	9	AV603964 Homo sapi
16	900	29.4	900	6	BD211249 Cloning a
17	611.2	19.9	692	9	HS3339407 Homo sapi
18	591.2	19.3	692	9	HS342408 Homo sapi
19	576.4	18.8	615	9	HS339459 Homo sapi

C 20	550.6	18.0	674	9	HSA330081	AJ330081 Homo sapi
C 21	487.8	15.9	703	9	HSA340216	AJ340216 Homo sapi
C 22	480.4	15.7	742	9	HSA340035	AJ340035 Homo sapi
C 23	478.6	15.6	807	9	HSA337736	AJ337736 Homo sapi
C 24	444.8	14.5	746	9	HSA341117	AJ341117 Homo sapi
C 25	443.8	14.5	701	9	HSA326768	AJ326768 Homo sapi
C 26	414.4	13.5	749	9	HSA323055	AJ323055 Homo sapi
C 27	411	13.4	693	9	HSA340953	AJ340953 Homo sapi
C 28	404.4	13.2	722	9	HSA340215	AJ340215 Homo sapi
C 29	402	13.1	681	9	HSA341310	AJ341310 Homo sapi
C 30	386	12.6	816	9	HSA340651	AJ340651 Homo sapi
C 31	338	11.0	602	6	BD211251	Cloning a
C 32	307	10.0	191949	2	AC109158	AC109158 Mus muscu
C 33	285.8	9.3	573	9	HSA341295	AJ341295 Homo sapi
C 34	283	9.2	283	6	AR168467	AR168467 Sequence
C 35	283	9.2	283	6	AR182284	AR182284 Sequence
C 36	283	9.2	283	6	AR303910	AR303910 Sequence
C 37	283	9.2	283	6	BD056681	BD056681 Galanin r
C 38	283	9.2	283	6	BD064652	BD064652 Human gal
C 39	283	9.2	283	6	BD064664	BD064664 Mouse gal
C 40	250.2	8.2	1351	5	AB095997	AB095997 Gallus ga
C 41	250.2	8.2	1703	5	AB095996	AB095996 Gallus ga
C 42	250.2	8.2	1751	5	AB095995	AB095995 Gallus ga
C 43	250.2	8.2	4121	5	AB095994	AB095994 Gallus ga
C 44	248.2	8.1	1050	6	BD222611	BD222611 Canine gr
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ALIGNMENTS

RESULT 1  
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LOCUS BD211242 3066 bp DNA linear PAT 17-JUL-2003  
DEFINITION Cloning and identification of motilin receptor.  
ACCESSION BD211242  
VERSION BD211242.1 GI:33021012  
KEYWORDS JP 2002517507-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3066)  
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macnei,D.,  
Howard,A.D., Pong,S.S. and Smith,R.G.  
TITLE Cloning and identification of motilin receptor  
JOURNAL Patent: JP 2002517507-A 1 18-JUN-2002;  
COMMENT MERCK AND CO INC  
OS Homo sapiens (human)  
PN JP 2002517507-A/1  
PD 18-JUN-2002  
PF 08-JUN-1999 JP 2000553444  
PR 12-JUN-1998 US 60/089098  
PI SCOTT D FEIGHNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI  
DOUGLAS MACNEIL,  
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH  
PC C07K14/705, A61K38/00, A61P1/00, C12N15/09, C12Q1/02, A61K37/02, PC  
C12N15/00  
CC Cloning and identification of motilin receptor. FH Key  
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ORIGIN

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Matches 3066; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CGAAACCCCTGACTACACAAAAAACAACAAAAATTTAGCGGGGCTTGGGCGCTCTGTGCTC 180  
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DB 361 GGTACGCTCCCTCCACCACTCGGCAATTTACAGAGAGGAGAACTGGGCTGGGCGAGACC 420  
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DB 841 CTAGCTCGGAGCGCTCTGAGCCACCCGAGAGCGCTTCTCGCGCCCCCGAGCGCA 900  
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DB 1021 GAGCACCATGGCAGCCCTTGAACCGGACGAGCGCCCGAGGGCGCGGAGCGCG 1080  
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3001	GGGGACACTCGGAGGAGACACGGTGGGCTACACCGGACAAGCGGCTAACGTTGAAGACGATG	3060
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3061	GGATAA 3066	

RESULT 2  
AL137000  
LOCUS  
DEFINITION  
AL137000 163284 bp DNA linear PRI 18-DEC-2000  
Human DNA sequence from clone RP1-203116 on chromosome 13 Contains  
the gene for KIAA0970 protein, COX7CP1 (cytochrome c oxidase  
subunit VIIC pseudogene 1), a novel pseudogene, the GPR38 (G  
protein-coupled receptor 38) gene, ESTs, STSs, GSSs and a CpG  
island, complete sequence.  
ACCESSION  
AL137000  
VERSION  
AL137000.6 GI:9944121

KEYWORDS	HTG; COX7Cp1; CpG island; cytochrome c oxidase; G protein-coupled receptor; GPR38; KIAA0970.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 163284)
AUTHORS	Wall, M.
TITLE	Direct Submission
JOURNAL	Submitted (18-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk request: clonerequest@sanger.ac.uk
COMMENT	On Aug 29, 2000 this sequence version replaced gi:9926419. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; ENBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at <a href="http://www.sanger.ac.uk/projects/C_elegans/wormpep">http://www.sanger.ac.uk/projects/C_elegans/wormpep</a> This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/Chr13">http://www.sanger.ac.uk/HGP/Chr13</a> IMPORTANT: This sequence is not the entire insert of clone RP11-203116 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-452110 is at 1 in this sequence. The true right end of clone RP11-103018 is at 163284 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-203116 is from the library RPc1-11.1 constructed by the group of Pieter de Jong. For further details see <a href="http://www.chori.org/bacpac/home.htm">http://www.chori.org/bacpac/home.htm</a>

FEATURES source

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41085. .41156
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/note="MIR2 repeat: matches 1. .42676"
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50979. .51656
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Db 143380 GAGGTGCGGGCGGGTGGACCCCTGGGTTCAGGAGTTCAGACCCAGGCTGCCACATGG 143439
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Db 143440 CGAAACCTGTACTACACAAAACACAAAATTTAGCCGGGGCTTGGCGCTCTGTGTCTC 143499
QY 181 CCAGCTTACTCAGAGGCTGAGGTGGAGGACTGCTTTGAGCCTGGGAGGTCCAGGCTGCAG 240
Db 143500 CCAGCTTACTCAGAGGCTGAGGTGGAGGACTGCTTTGAGCCTGGGAGGTCCAGGCTGCAG 240
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QY	2579	TTTTTTCTGGGGTGAGGATCTGCTAGGTAGAAAGTTTCTCTAAATTTATTTTCTGCTGTTAC	2638
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QY	2879	ACCCAATCTCTACAACTCATTTCAAGAAGTACAGAGCGCGGCTTTAAACTGCTGC	2938
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LOCUS			
DEFINITION		Homo sapiens chromosome 13 clone RP11-804, 3 unordered pieces.	
ACCESSION		AL596304	
VERSION		AL596304.3	GI:15147703
KEYWORDS		HTG; HTGS_PHASE1; HTGS_CANCELLED.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Clark, G.	
TITLE		Direct Submission	
JOURNAL		Submitted (08-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk	
COMMENT		On Aug 10, 2001 this sequence version replaced gi:15131387.	
		----- Genome Center	
		Center: Sanger Centre	
		Center code: SC	
		Web site: http://www.sanger.ac.uk	
		Contact: humquery@sanger.ac.uk	
		----- Project Information	
		Center project name: bA804	
		----- Summary Statistics	
		Assembly program: XGAP4; version 4.5	
		Sequencing vector: plasmid; L08752; 100% of reads	
		Chemistry: Dye-terminator Big Dye; 100% of reads	
		Consensus quality: 149716 bases at least Q40	
		Consensus quality: 150039 bases at least Q30	
		Consensus quality: 150247 bases at least Q20	

Insert size: 341360; sum-of-contigs									
Insert size: 157238; 2.0% error; agarose-fp									
Quality coverage: 3.92x in Q20 bases; sum-of-contigs Quality									
coverage: 8.77x in Q20 bases; agarose-fp									
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* NOTE: This is a 'working draft' sequence. It currently									
* consists of 3 contigs. The true order of the pieces									
* is not known and their order in this sequence record is									
* arbitrary. Gaps between the contigs are represented as									
* runs of N, but the exact sizes of the gaps are unknown.									
* This record will be updated with the finished sequence									
* as soon as it is available and the accession number will									
* be preserved.									
* 1 146853: contig of 146853 bp in length									
* 146854 146953: gap of 100 bp									
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QY	241	TGAGCTGTGATCGCGCCACTTAAACTCCAGCTC	GACAGTTC	AGAGTTCG	AGTCTCTCAAGA	300			
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QY	301	AGAAAAAAGAAAGAAAGAAAGAAAGAAATTT	TGCTCAAT	TATAT		360			
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QY	361	GGTCAGTCTCCCTCCACCACTCGCGAATTTAC	AGAGAGG	AGAACTGG	CGCGAGACC	420			
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QY	421	AGGACTAGCCCAAGATTACAAAGTTACTCGGT	TGTAGAG	CCAGATTAG	CAGGAGG	480			
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QY	481	CTCTAGATCTTGCTAGACTCCCTCTATTATT	TAGCATT	TGCTTCT	TGAGGATTA	540			
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Db	321456	GGTTGCCCTTCCACGTTGGCGAATATTTACATAAACACGGAAGATTTCGGCGATGATGT	321515			
Qy	2819	ACTTCTCTCAGTACTTTAAGATCGTCCCTCGAATTTTCTATCTGACGCATCTATCA	2878			
Db	321516	ACTTCTCTCAGTACTTTAAGATCGTCCCTCGAATTTTCTATCTGACGCATCTATCA	321575			
Qy	2879	ACCCAAATCTCTACAACTCATTTCAAAGAAGTACAGAGCGCGGCTTTAAACTGCTGC	2938			
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Qy	2939	TGCGAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAACGAGGACACTCGGGGGAAGTTG	2998			
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Qy	2999	CAGGGGACACTGGAGGAGACACGGTGGGCTACACCGAGACAAAGCGCTAAACGTAAGACGA	3058			
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LOCUS	AX711879	349980 bp	DNA linear PAT 08-MAY-2003			
DEFINITION	Sequence 1 from Patent WO03000727.					
ACCESSION	AX711879					
VERSION	AX711879.1	GI:29787684				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
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	Zhang, Y., Moffatt, M., Cookson, W. and Tinsley, J.O.					
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AUTHORS	Patent: WO 03000727-A 1 03-JAN-2003;					
JOURNAL	ISIS INNOVATION LIMITED (GB)					
FEATURES	Location/Qualifiers					
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[illegible]



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QY	2159	CCCGGATCCGATTCAGTACACGAGCTGCTTTCCAGAGCTCTGAGACCAAGAGGAGA	2218
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LOCUS			

DEFINITION	Homo sapiens orphan G protein-coupled receptor (GPR38) gene, complete cds.
ACCESSION	AF034632
VERSION	AF034632.1 GI:2654158
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 2040)
AUTHORS	McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D., Hreniuk, D.L., Smith, R.G., Howard, A.D. and Van der Ploeg, L.H.
TITLE	Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors
JOURNAL	Genomics 46 (3), 426-434 (1997)
MEDLINE	98110578
PUBMED	9441746
REFERENCE	2 (bases 1 to 2040)
AUTHORS	McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D., Hreniuk, D.L., Smith, R.G., Van Der Ploeg, L.H.T. and Howard, A.D.
TITLE	Direct Submission
JOURNAL	Submitted (12-NOV-1997) Biochemistry and Physiology, Merck and Co., Inc., PO Box 2000, Rahway, NJ 07065, USA
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QY	1089 GCGTTCGCGCTTCGAGACGAGCGCGCTTCGCGCCCTTTCCCTCGGGGGCGCTGGTGGCG 1148
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Db 1501 AGCCTACTATCGAGTTTAAAGCAAGTATCCATCGAGCCTGCGAGCCTGTCATTTTTTCT 1560
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QY 2707 GGTCTGTGCTTATGTTCAGTGGTGGTCTGCGATTTTATTAATTTGCTGGTTGCC 2766
Db 1681 GGTCTGTGCTTATGTTCAGTGGTGGTCTGCGATTTTATTAATTTGCTGGTTGCC 1740
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QY 2947 AAGTCCAGCGCGAGAGGCTTCCACAGAGCAGGAGACACTGCGGGGAGTTGCGAGGGAC 3006
Db 1921 AAGTCCAGCGCGAGAGGCTTCCACAGAGCAGGAGACACTGCGGGGAGTTGCGAGGGAC 1980
QY 3007 ACTGAGGAGACACGTTGGGCTACACCGAGACAGCGCTAACTGTAAGACGATGGGATAA 3066
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RESULT 7
AX154591
LOCUS AX154591 1161 bp DNA linear PAT 23-JUN-2001
DEFINITION Sequence 11 from Patent WO0138355.
ACCESSION AX154591
VERSION AX154591.1 GI:14536177
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.
TITLE Method of forming a peptide-receptor complex with zsi933 and
        therapeutic use thereof
JOURNAL Patent: WO 0138355-A 11 31-MAY-2001;
        ZymoGenetics, Inc. (US)
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ORIGIN

Query Match 33.9%; Score 1038; DB 6; Length 1161;  
Best Local Similarity 99.8%; Pred. No. 8e-153;  
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1029 ATGGGACGCCCTGGAACGGCAGCGACCGCCCGGAGGGGGCGGAGCGCCGCGTGGGCC 1088  
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Qy 1149 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208  
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Qy 1329 TCGGGCCCTGGGTGTTGGGGCGCTGCTGCGCGCTGCTGCGCGCTGCTGCGCGCTGCTG 1388  
Db 301 TCGGGCCCTGGGTGTTGGGGCGCTGCTGCGCGCTGCTGCGCGCTGCTGCGCGCTGCTG 360

Qy 1389 TGCACCTAGCCACGCTGTCACATGACCGGCTGACGCTGACGCTGACGCTGACGCTG 1448  
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Qy 1449 TCGCGCCGCTCGCGCCGCTGTTGCTGACCGCGCGCGCTGCGCGCGCTCATGCT 1508  
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RESULT 8  
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LOCUS BD211244 1390 bp DNA linear PAT 17-JUL-2003  
DEFINITION Cloning and identification of motilin receptor.  
ACCESSION BD211244  
VERSION BD211244.1 GI:33021014  
KEYWORDS JP 2002517507-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1390)  
AUTHORS Feighner, S.D., Patchett, A.A., Tan, C., McKee, K., Macnei, D.,  
Howard, A.D., Pong, S.S. and Smith, R.G.  
TITLE Cloning and identification of motilin receptor  
JOURNAL Patent: JP 2002517507-A 3 18-JUN-2002;  
MERCK AND CO INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002517507-A/3  
PD 18-JUN-2002  
PF 08-JUN-1999 JP 2000553444  
PR 12-JUN-1998 US 60/089098  
PI SCOTT D FEIGHNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI  
DOUGLAS MACNEIL,  
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH  
PC C07K14/705, A61K38/00, A61P1/00, C12N15/09, C12Q1/02, A61K37/02, PC  
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Best Local Similarity 99.8%; Pred. No. 8e-153;  
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1029 ATGGGACGCCCTGGAACGGCAGCGACCGCCCGGAGGGGGCGGAGCGCCGCGTGGGCC 1088  
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Qy 1089 GCGTGGCGCCTTGGCAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGCTGCGG 1148  
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Qy 1149 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208  
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

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QY 1869 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGCGACCGGACAGCGTCCGCGTCTG 1928
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QY 1929 C 1929
Db 901 C 901

RESULT 10
LOCUS CQ724376 1239 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 10310 from Patent WO02068579.
ACCESSION CQ724376
VERSION CQ724376.1 GI:42285233
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE Kite, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 10310 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1509 GTGCTGTGGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1568
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QY 1809 CTGTGCTCAGCATCTCTACCGGCTCATCGGGCGGAGCTGTGAGAGCGCGGCGCG 1868
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QY 1869 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTCCGCGTCTG 1928
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QY 1929 C 1929
Db 901 C 901

RESULT 11
LOCUS CQ831648 1239 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1 from Patent WO2004057328.
ACCESSION CQ831648
VERSION CQ831648.1 GI:50831561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Golz,S., Brueggemeier,U. and Summer,H.
TITLE Diagnostics and therapeutics for diseases associated with
g-protein-coupled receptor 38 (gpr38)
JOURNAL Patent: WO 2004057328-A 1 08-JUL-2004;
Bayer HealthCare AG (DE)
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Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ZymoGenetics, Inc. (US)  
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JOURNAL  
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Query Match 29.4%; Score 901; DB 6; Length 1239;  
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LOCUS AX154589 1239 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 9 from Patent WO0138355.  
ACCESSION AX154589  
VERSION AX154589.1 GI:14536175  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.  
AUTHORS Method of forming a peptide-receptor complex with zslg33 and  
TITLE

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Db 901 C 901

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LOCUS AX549187 1239 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 472 from Patent WO02061087.
ACCESSION AX549187
VERSION AX549187.1 GI:25813904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 472 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Query Match 29.4%; Score 901; DB 6; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14
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LOCUS AX572965 1239 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 1 from Patent WO02057791.
ACCESSION AX572965
VERSION AX572965.1 GI:26005013
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Brown,J.P., Burmer,G.C., Roush,C.L. and Kulander,B.G.
TITLE Diagnostic and therapeutic compositions and methods related to gpr
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JOURNAL Patent: WO 02057791-A 1 25-JUL-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
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ORIGIN
Query Match 29.4%; Score 901; DB 6; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1029 ATGGCAGCCCTGTGAACCGGAGCAGCGCGCCCGAGGGGGCGCGGAGCCCGTGGGCC 1088
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QY	1749	CAGCTGGCGCGCTGCGTGTCTATGCTGTGGGTACACCGCCTACTTCTTCTGCGCCTTT	1808
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OM nucleic - nucleic search, using sw model

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
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- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1239	100.0	1239	6	CQ724376 Sequence
3	1239	100.0	1239	6	CQ831648 Sequence
4	1239	100.0	1239	6	AX154589 Sequence
5	1239	100.0	1239	6	AX549187 Sequence
6	1239	100.0	1239	6	AX572965 Sequence
7	1239	100.0	1239	9	AY603964 Homo sapi
8	1078	87.0	1390	6	BD211244 Cloning a
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13	901	72.7	341560	2	AL596304 Homo sapi
14	901	72.7	349980	6	AX711879 Sequence
15	901	72.7	349980	6	AX739961 Sequence
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23	283	22.8	283	6	AR168467	AR168467 Sequence
24	283	22.8	283	6	AR182284	AR182284 Sequence
25	283	22.8	283	6	AR303910	AR303910 Sequence
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ALIGNMENTS

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LOCUS BD211243 1239 bp DNA linear PAT 17-JUL-2003  
DEFINITION Cloning and identification of motilin receptor.  
ACCESSION BD211243  
VERSION BD211243.1 GI:33021013  
KEYWORDS JP 2002517507-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (Bases 1 to 1239)  
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., Mcke, K., Macnei,D.,  
Howard,A.D., Pong,S.S. and Smith,R.G.  
TITLE Cloning and identification of motilin receptor  
JOURNAL Patent: JP 2002517507-A 2 18-JUN-2002;  
COMMENT MERCK AND CO INC  
OS Homo sapiens (human)  
PN JP 2002517507-A/2  
PD 18-JUN-2002  
PF 08-JUN-1999 JP 2000553444  
PI 12-JUN-1998 US 60/089098  
PI SCOTT D FEIGHNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI  
DOUGLAS MACNEIL,  
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH  
PC C07K14/705, A61K38/00, A61P1/00, C12N15/09, C12Q1/02, A61K37/02, PC  
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Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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LOCUS	CQ831648	1239 bp	DNA linear PAT 29-JUL-2004
DEFINITION	Sequence 1 from Patent WO2004057328.		
ACCESSION	CQ831648		
VERSION	CQ831648.1	GI:50831561	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Golz, S., Brueggemeier, U. and Summer, H.		
TITLE	Diagnostics and therapeutics for diseases associated with g-protein-coupled receptor 38 (gpr38)		
JOURNAL	Patent: WO 2004057328-A 1 08-JUL-2004; Bayer HealthCare AG (DE)		
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LOCUS AX154589 1239 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 9 from Patent WO0138355.  
ACCESSION AX154589  
VERSION AX154589.1 GI:14536175

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Sheppard, P. O., Jaepers, S. R., Deisher, T. A. and Bishop, P. D.  
TITLE Method of forming a peptide-receptor complex with zsig33 and  
JOURNAL therapeutic use thereof  
Patent: WO 0138355-A 9 31-MAY-2001;  
ZymoGenetics, Inc. (US)

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Query Match 100.0%; Score 1239; DB 6; Length 1239;  
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## ORIGIN

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AX549187
LOCUS AX549187 1239 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 472 from Patent WO02061087.
ACCESSION AX549187
VERSION AX549187.1 GI:25813904
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 472 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 3.2e-155;
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AX572965 1239 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 1 from Patent WO02057791.
ACCESSION AX572965
VERSION AX572965.1 GI:26005013
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Brown,J.P., Burner,G.C., Roush,C.L. and Kulander,B.G.
TITLE Diagnostic and therapeutic compositions and methods related to gpr
38
JOURNAL Patent: WO 02057791-A 1 25-JUL-2002;
Lifespan Biosciences, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 3.2e-155;
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	181	ATGCTGATCGGGCGCTACCGGGACATCGGACACCGACCACTTTGTATCTTGGGAGCATG	240
Qy	241	GCGGTGCGGACCTACTCATCTGCTCGGGCTGCGGTTGAGCTGTACCGCTCTGCGGC	300
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DEFINITION	AY603964	Homo sapiens motilin/ghrelin receptor mRNA, complete cds.	
ACCESSION	AY603964		
VERSION	AY603964.1	GI:47571310	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	King, M.M., Aronstam, R.S. and Sharma, S.V.		
TITLE	Isolation of cDNA coding for motilin/ghrelin receptor (MTLR1/GPR38)		
JOURNAL	Unpublished		
REFERENCE			
AUTHORS	King, M.M., Aronstam, R.S. and Sharma, S.V.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-APR-2004) Guthrie cDNA Resource Center, Guthrie		
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RESULT 8  
BD211244  
LOCUS BD211244 1390 bp DNA linear PAT 17-JUL-2003  
DEFINITION Cloning and identification of motilin receptor.  
ACCESSION BD211244  
VERSION BD211244.1 GI:33021014  
KEYWORDS JP 2002517507-A/3.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 1390)  
Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macnei,D.,  
Howard,A.D., Pong,S.S. and Smith,R.G.  
TITLE Cloning and identification of motilin receptor  
JOURNAL Patent: JP 2002517507-A 3 18-JUN-2002;  
MERCK AND CO INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002517507-A/3  
PD 18-JUN-2002  
PF 08-JUN-1999 JP 2000553444  
PR 12-JUN-1998 US 60/089098  
PI SCOTT D FEIGHNER,ARTHUR A PATCHETT,CARINA TAN,KAREN MCKEE, PI  
DOUGLAS MACNEIL,  
PI ANDREW D HOWARD,SHENG SHUNG PONG,ROY G SMITH  
PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC  
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## RESULT 9

AX154591  
LOCUS AX154591 1161 bp DNA linear PAT 23-JUN-2001  
DEFINITION Sequence 11 from Patent WO0138355.  
ACCESSION AX154591  
VERSION AX154591.1 GI:14536177  
KEYWORDS

## SOURCE

Homosapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.  
AUTHORS Method of forming a peptide-receptor complex with zslg33 and  
TITLE

therapeutic use thereof  
Patent: WO 0138355-A 11 31-MAY-2001;  
ZymoGenetics, Inc. (US)  
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## ORIGIN

Query Match 72.7%; Score 901; DB 6; Length 1161;  
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Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
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Qy 541 CAGGACCCCGGCTCTCCGTAGTCCCGGGCTCAATGGACACCGCGGAGTACGCTCTCTCG 600  
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Qy 601 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
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Qy 661 GGGCGCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 661 GGGCGCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720



\_\_\_\_\_

The true right end of clone RP11-103J18 is at 163284 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unSURE' feature key. RP11-203J16 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pBACE3.6.

## FEATURES

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DEFINITION	AXT39961		
ACCESSION	AXT39961.1	GI:30519236	
VERSION			
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	Zhang, Y., Moffatt, M. and Cookson, W.	
AUTHORS		Treatment and diagnosis of B cell chronic lymphocytic leukaemia	
TITLE		Patent: WO 03000296-A 1 03-JAN-2003;	
JOURNAL		ISIS INNOVATION LIMITED (GB)	
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ORIGIN			
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Best Local Similarity 100.0%; Pred. No. 5.5e-111;			
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	121	GTGACCGCTGTGTGCTGTGCTGCTGCTGCGGGTGAGCGGCAACGTGTGACCGCTG	180
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Qy	181	ATGCTGATCGGCGCTACCGGGAATCGCGACCAACCAACTGTACCTGGGCGAGCATG	240
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Qy	241	GCCGTGTCGACCTACTCATCTGCTCGGCGTTCGCTGCTACCTGTACCGCTCTGGCGC	300
Db	38256	GCCGTGTCGACCTACTCATCTGCTCGGCGTTCGCTGCTACCTGTACCGCTCTGGCGC	38315

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 11, 2005, 13:13:41 ; Search time 66.6015 Seconds  
(without alignments)  
3167.746 Million cell updates/sec

Title: US-09-719-485-3  
Perfect score: 2155  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2155.0	100.0	412	1	MTLR_HUMAN	O43193 homo sapien
2	907.0	42.1	363	2	O93413	O93413 spherooides
3	895.0	41.5	385	2	O6YGGZ	O6YGGZ acanthopagr
4	864.5	40.1	366	1	GHSR_PIG	O95254 sus scrofa
5	863.5	40.1	366	1	GHSR_HUMAN	O92847 homo sapien
6	863.0	40.0	360	2	O6B7N9	O6B7N9 macaca fasc
7	861.5	40.0	364	1	GHSR_MOUSE	O99P50 mus musculus
8	861.5	40.0	364	1	GHSR_RAT	O08725 rattus norv
9	855.0	39.7	347	2	O7ZT14	O7ZT14 gallus gall
10	851.0	39.5	374	2	O93412	O93412 spherooides
11	825.5	38.3	366	2	O8MHZ5	O8MHZ5 oris aries
12	759.0	35.2	331	2	O7ZJZ9	O7ZJZ9 gallus gall
13	671.0	31.1	295	2	O6YGGZ	O6YGGZ acanthopagr
14	643.0	28.8	267	2	O7ZJZ8	O7ZJZ8 gallus gall
15	608.0	28.2	559	2	O93414	O93414 spherooides
16	535.0	24.8	211	2	O711Q8	O711Q8 gallus gall
17	501.0	23.2	424	1	NTR1_RAT	P20789 rattus norv
18	499.5	23.2	424	1	NTR1_MOUSE	O88319 mus musculus
19	497.0	23.1	418	1	NTR1_HUMAN	P30989 homo sapien
20	487.5	22.6	426	2	O8NE20	O8NE20 homo sapien
21	485.5	22.5	215	2	O711Q7	O711Q7 gallus gall
22	485.5	22.5	403	2	O7LDP6	O7LDP6 homo sapien
23	485.5	22.5	426	2	O9HB89	O9HB89 homo sapien
24	478.5	22.2	395	2	O91Z76	O91Z76 mus musculus
25	478.5	22.2	395	2	O8BZ39	O8BZ39 mus musculus
26	477.5	22.2	395	2	O9JIB1	O9JIB1 rattus norv
27	477.0	22.1	415	2	O96AM5	O96AM5 homo sapien
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DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DE	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Motilin receptor (G protein-coupled receptor 38)			
GN	Name=MLNR; Synonyms=GPR38, MTLR, MTLR1, Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
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RX	MEDLINE=98110578; PubMed=9441746; DOI=10.1006/geno.1997.5069;			
RA	McKee K.K., Tan C.P., Palya O.C., Liu J., Feighner S.D., Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;			
RA	"Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors.";			
RL	Genomics 46:426-434(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS A AND B).			
RX	MEDLINE=99316084; PubMed=10381885; DOI=10.1126/science.284.5423.2184;			
RA	Feighner S.D., Tan C.P., McKee K.K., Palya O.C., Hreniuk D.L., Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A., Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S., O'Neill G., van der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G., Howard A.D.;			
RA	"Receptor for motilin identified in the human gastrointestinal system.";			
RL	Science 284:2184-2188(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15057823; DOI=10.1038/nature02379;			
RA	Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L., Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E., Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E., Ashwell R.I.S., Babbage A.K., Baguley C.L., Bailey J., Bannerjee R., Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S., Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P., Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M., Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J., DeLoukas P., Dhumi P., Dunham I., Dunn M., Earthrowl M.E., Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L., Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J., Grafham D.V., Griddle S.M., Griffiths C., Hall R.E., Hammond S., Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J., Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M., King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A., Lloyd D.M., Lloyd C., Loveland J.B., Lovell J., Martin S., Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,			

O7qeg8 anopheles g  
O65y84 bombyx mori  
O55040 mus musculus  
O7p2f2 anopheles g  
O8tc7 drosophila  
O17239 caenorhabdi  
O6vyh4 heliothis z  
O9vfn4 drosophila  
O8tc9 drosophila  
O7kek4 drosophila  
O7qbc1 anopheles g  
O8tld0 drosophila  
O6wnx7 drosophila  
O9vfw6 drosophila

RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,  
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,  
RA Sehra H.K., Showkneen R., Skuce C.D., Smith M., Steward C.A., Tubby B.,  
RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Wally D.L.,  
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,  
RA Wilming L., Wray P.M., Wright M.W., Young L., Coulson A., Durbin R.,  
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,  
RT Nature 428:522-528 (2004).  
RL The DNA sequence and analysis of human chromosome 13.  
RN (4)  
RP FUNCTION.  
RX MEDLINE=21219832; PubMed=11322507; DOI=10.1385/ENDO.14.1.009;  
RA Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,  
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;  
RA "Growth hormone secretagogue receptor family members and ligands."  
RT Endocrine 14:9-14 (2001).  
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CC -!- ALTERNATIVE PRODUCTS:  
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CC IsoId=O43193-1; Sequence=Displayed;  
CC Name=B;  
CC IsoId=O43193-2; Sequence=VSP 001894;  
CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone marrow.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
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CC EMBL; AL137000; CAC19107.1; -;  
CC Genew; HGNC:4495; MLNR.  
CC MIM; 602885; -;  
CC GO; GO:0005987; C:integral to plasma membrane; TAS.  
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
CC GO; GO:0007586; P:digestion; TAS.  
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm1.1; 1.  
CC PRINTS; PR00237; GPCRRHODPSN.  
CC PROSITE; PS00237; G PROTEIN RECP FL\_1; 1.  
CC PROSITE; PS0262; G PROTEIN RECP FL\_2; 1.  
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;  
KW Transmembrane.  
FT DOMAIN 1 35 Extracellular (Potential).  
FT TRANSMEM 36 56 1 (Potential).  
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FT TRANSMEM 75 94 2 (Potential).  
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FT TRANSMEM 113 134 3 (Potential).  
FT DOMAIN 135 157 Cytoplasmic (Potential).  
FT TRANSMEM 158 178 4 (Potential).  
FT DOMAIN 179 246 Extracellular (Potential).  
FT TRANSMEM 247 270 5 (Potential).  
FT DOMAIN 271 298 Cytoplasmic (Potential).  
FT TRANSMEM 299 320 6 (Potential).  
FT DOMAIN 321 334 Extracellular (Potential).  
FT TRANSMEM 335 358 7 (Potential).  
FT DOMAIN 359 412 Cytoplasmic (Potential).  
FT DISULFID 111 235 By similarity.  
FT CARBOHYD 6 6 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 192 192 N-linked (GlcNAc. . .) (Potential).  
FT VARSPPLIC 301 412 LVVLAFLICWLPFHVGRRIIYINTEDSRMVFSQYFNIVAL  
SRDTAGEVADTGCGTGVGTETSAVNKTWG -> RKWSRRG  
SKDACIQSPGPGTAQTGLPLLAQLWAPLPAPFPISIPAS

FT TRRGSGGIYNLLVALPRQWHLKHGRFADDDLLSVL  
FT (in isoform B).  
FT /FTId=VSP\_001894.  
SQ SEQUENCE 412 AA; 45344 MW; CL3PF6165012DEF3 CRC64;  
Query Match 100.0%; Score 2155; DB 1; Length 412;  
Best Local Similarity 100.0%; Pred. No. 9.4e-135;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPLGALVPTAVCLCLFVVGVSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPLGALVPTAVCLCLFVVGVSGNVTV 60  
Qy 61 MLIGRYDMRTTNTLYLGSMVAVSDLLILGLPFDLYLWRSRPWVFGPLLCRLSLYYVGE 120  
Db 61 MLIGRYDMRTTNTLYLGSMVAVSDLLILGLPFDLYLWRSRPWVFGPLLCRLSLYYVGE 120  
Qy 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLAIVLMAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLAIVLMAVALLSAGPFLVGV 180  
Qy 181 QDPGISVVGNGTARTIASSPLASSPPLWLSRAPSPSPGPTAAALFSSRECRSPA 240  
Db 181 QDPGISVVGNGTARTIASSPLASSPPLWLSRAPSPSPGPTAAALFSSRECRSPA 240  
Qy 241 QLGALRVMLVTTAYFFLPFLCLISILYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300  
Db 241 QLGALRVMLVTTAYFFLPFLCLISILYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300  
Qy 301 LVVLAFLICWLPFHVGRRIIYINTEDSRMVFSQYFNIVALQLFYLSASINPILYNLSK 360  
Db 301 LVVLAFLICWLPFHVGRRIIYINTEDSRMVFSQYFNIVALQLFYLSASINPILYNLSK 360  
Qy 361 KYRAAFKLLARKSRPRGHSRDTAGEVADTGCGTGVGTETSAVNKTWG 412  
Db 361 KYRAAFKLLARKSRPRGHSRDTAGEVADTGCGTGVGTETSAVNKTWG 412  
RESULT 2  
O93413 PRELIMINARY; PRT; 363 AA.  
ID O93413  
AC O93413  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Orphan G protein-coupled receptor.  
OS Spherooides nephelus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Spherooides.  
OX NCBI\_TaxID=39110;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20092336; PubMed=10628755; DOI=10.1210/me.14.1.160;  
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,  
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Margund R.,  
RA Patchett A.A., Howard A.D., Smith R.G.;  
RT "Ligand activation domain of human orphan growth hormone (GH)  
secretagogue receptor (GHS-R) conserved from Pufferfish to humans."  
RL Mol. Endocrinol. 14:160-169 (2000).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC EMBL; AF082210; AAC33473.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . . ; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.  
DR InterPro; IPR003905; GHS1\_receptor.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm1.1; 1.  
DR PRINTS; PR01417; GHSRECEPTOR.

```
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 363 AA; 41324 MW; 74518BD9CD310991 CRC64;

Query Match 42.1%; Score 907; DB 2; Length 363;
Best Local Similarity 50.6%; Pred. No. 3e-52;
Matches 180; Conservative 56; Mismatches 76; Indels 44; Gaps 5;

QY 31 SPEPLGALVPVAVCLCLFVGVGSGVNTVMLIGRYDMRTTNNLYLGSMAVSDLLILLG 90
DB 31 SLFPASTLIPVTVICILFVVGVTGNTMTILIQYFKOMKTTNNLYLGSMAVSDLVFLC 90

QY 91 LPFDLYRLWRSRPWPGFLLCRSLYVGEQCTYATLLHMTALSVERYLAICRPLRVLV 150
DB 91 LPFDLYRLWKYVPLFGEAVCLHYIFEGCTSAITLHMTALSVERYLAISPLRSKQV 150

QY 151 TRRRVRLIAVLWALLSAGFLVGVQDPGIVVPLGNGTARIASSPIASSPPLWL 210
DB 151 TRRRVQYIILALWCFALVSAAPTLFLVGVEYD-----NET----- 185

QY 211 SRAPPSPPSPETAEEAALFSSRECRPSPAQL--GALRVMLVMTTAYRFLPCLLSILY 268
DB 186 ----HPDNTG-----QCKHTGYALSSQGLHIMVSTYFFCPMLCLFLY 229

QY 269 LIGRELWSSRRPLRGPAASGRGRHRTQVRLVLLVVLAFIICWLPFHVGRIIYINTEDSR 328
DB 230 SIGCKLWKSNDLOGPCALARESHRQTVKILVVVVLAFIICWLPYHIGRNLFAQVDDYD 289

QY 329 MMYSQYFNIVALQFLYLSASINPILYNLISKYRAAFAFKLLARKSRPRGRHRSR 384
DB 290 TAMLSONFNMAWMVLCYLSASINPVVYMLMSRYRAAKRLLHQ-RPKPAHRQ 344

RESULT 3
Q5IGZ3
ID Q6YGZ3 PRELIMINARY; PRT; 385 AA.
AC Q6YGZ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Growth hormone secretagogue receptor la.
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;
RA Chan C.B., Cheng C.H.K.;
RT "Identification and functional characterization of two alternatively
spliced growth hormone secretagogue receptor transcripts from the
pituitary of black seabream Acanthopagrus schlegelii."
RL Mol. Cell. Endocrinol. 214:81-95(2004).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY151040; AAN77875.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . . IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
DR InterPro; IPR0033905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.

SQ SEQUENCE 385 AA; 43697 MW; 665CBDA9702887A9 CRC64;

Query Match 41.5%; Score 895; DB 2; Length 385;
Best Local Similarity 45.7%; Pred. No. 2e-51;
Matches 191; Conservative 62; Mismatches 99; Indels 66; Gaps 11;

QY 17 PFWPALPPCDERRCS-----PPPLG-----ALVPVAVCLCLFVGVGSGNV 57
DB 2 PSWPNLSECLSLNCSWEETRNRATKFDGLPLPLNYYSIPLLTGTITACTLLFLVGVAGNV 61

QY 58 VTVMILIGRYDMRTTNNLYLGSMAVSDLLILLGPPDLYRLWRSRPWPGFLLCRSLYLV 117
DB 62 MTLVLYKYRDMRTTNNLYLGSMAVSDLLIFCLPDLIDLYRMWRYRPNRFGDCKLFOFV 121

QY 118 GEGCTYATLLHMTALSVERYLAICRPLRVLVTRRRVRLIAVLWALLSAGFPLFLV 177
DB 122 SESCTYSTILSITALSVERYLAICFPLRAKALVTKERVALLLLMTVYLSLSAGPFVNV 181

QY 178 GVEQD---PGISVVPGLNGTARIASSPIASSPPLWLSRAPPPSPGSPETAAALFSRE 234
DB 182 GVERDSMMWPGNLSWVGNGTGFF-----PEEGD-----TRE 212

QY 235 CRPS--PAQLGALRVMLVMTTAYRFLPCLLSILYGLIGRELWSSRRPLR-GPAASGRER 291
DB 213 CKMTHYAVESGUMGAMVWLVSSVFFPMPVFCVLTVLSLIGRLMQHRRTNINSRVHREK 272

QY 292 GHRQTVRLVLLVVLAFIICWLPFHVGRIIYINTEDS---RMYSQYFNIVALQFLYLSA 348
DB 273 SNRQTIKMLVVVVLAFVLCWLPFHVGRLQFSLDAPSLLSLSEYCSLVSVVLYLSA 332

QY 349 SINPILYNLISKYRAAFAFKLL-LARKSRPRGRHRSRDTAGEVAGDTGGDTVGYTETS 405
DB 333 AINPILYNIMSKYRGAARLFLGLIDSQPRG-----RTASTVKGDGNS---GWTEST 382

RESULT 4
GHSR_PIG
ID GHSR_PIG STANDARD; PRT; 366 AA.
AC Q95254; Q95255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=GHSR;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RX STRAIN=Yorkshire; TISSUE=Pituitary;
RA MEDLINE=96337998; PubMed=8688086;
RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberato P.A.,
Rosenblum C.I., Hamelin M., Hreniuk D.L., Palyha O.C., Anderson J.,
Paresse P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S.,
Chang L.-Y., Elbrecht A., Dashkevich M., Heavens R., Rigby M.,
Sirinathsinghji D.J.S., Dean D.C., Melillo D.G., Patchett A.A.,
Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M.,
Smith R.G., van der Ploeg L.H.T.;
RT "A receptor in pituitary and hypothalamus that functions in growth
hormone release."
RL Science 273:974-977(1996).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
stimulates growth hormone secretion. Binds also other growth
hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
as well as non-peptide, low molecular weight secretagogues (e.g.
L-692,429, MK-0677, adenosine).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1A;
IsoId=Q95254-1; Sequence=Displayed;
```







Db 213 IFFFLPVCLTVLYSLGKLRERRRDAVVCASLRDQNHQTVKMLAVVFAFLCWLP 272  
 Qy 314 FHVGRIIYNTEDS---RMVFSQYFNVAIQLFVLSASINPILNLSKYYRAAFKLL 370  
 Db 273 FHVGRIYFSKSPGSLGSLAQISQYCNLSVFLVFLSAAINPILNLSKYYRAAFKLL 332  
 Qy 371 LARKSRPGRFHRSTAGEVAGDTGGDTVGTETSAN 407  
 Db 333 GFEPFSQRKSLTKDESSR-----AMTESSIN 359

## RESULT 7

CHSR\_MOUSE  
 ID CHSR\_MOUSE STANDARD; PRT; 364 AA.  
 AC Q99P50; QB8WX9; Q91282;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing  
 DE peptide receptor) (GHRP) (Ghrelin receptor).  
 GN Name=Ghr;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kandi A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongsaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,  
 RA Petrowsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RT Nature 420:563-573 (2002).  
 RN [2]  
 RP SEQUENCE OF 1-183 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
 RA Kacsoh B.;  
 RT "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by  
 RT rapid amplification of cDNA ends (RACE).";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 73-257 FROM N.A.  
 RC STRAIN=129S3/SvImJ;  
 RA Peng X., Frohman L.A., Kineman R.D.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.  
 CC Stimulates growth hormone secretion. Binds also other growth

hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)  
 as well as non-peptide, low molecular weight secretagogues (e.g.  
 L-692,429, MK-0677, adenosine) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AK049671; BAC33866.1; -;  
 CC EMBL; AY056474; AAL13336.1; -;  
 CC EMBL; AF332997; AAG61141.1; -;  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm.1; 1.  
 CC PRINTS; PR00237; GPCRHHODOPS.  
 CC PROSITE; PS00237; G PROTEIN RECP Fl\_1; 1.  
 CC PROSITE; PS0262; G-PROTEIN RECP Fl\_2; 1.  
 CC G-protein coupled receptor; Glycoprotein; Transmembrane.  
 KW DOMAIN 1 40 Extracellular (Potential).  
 FT TRANSMEM 41 66 1 (Potential).  
 FT DOMAIN 67 72 Cytoplasmic (Potential).  
 FT TRANSMEM 73 96 2 (Potential).  
 FT DOMAIN 97 117 Extracellular (Potential).  
 FT TRANSMEM 118 139 3 (Potential).  
 FT DOMAIN 140 162 Cytoplasmic (Potential).  
 FT TRANSMEM 163 183 4 (Potential).  
 FT DOMAIN 184 211 Extracellular (Potential).  
 FT TRANSMEM 212 235 5 (Potential).  
 FT DOMAIN 236 263 Cytoplasmic (Potential).  
 FT TRANSMEM 264 285 6 (Potential).  
 FT DOMAIN 286 302 Extracellular (Potential).  
 FT TRANSMEM 303 326 7 (Potential).  
 FT DOMAIN 327 364 Cytoplasmic (Potential).  
 FT DISULFID 115 197 By similarity.  
 FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 59 59 G -> S (in Ref. 2).  
 SQ SEQUENCE 364 AA; 40969 MW; 8F1214E58EF3B2E8 CRC64;  
 Query Match 40.0%; Score 861.5; DB 1; Length 364;  
 Best Local Similarity 48.3%; Pred No. 3.1e-49;  
 Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;  
 Qy 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPFLGALVPVTVAVCLFVVGVS 55  
 Db 2 WNAT--PSEEPNPVTLDDWDASPGNDSLSDELLPLFPAPLLAGVATCATVALFVVGIS 59  
 Qy 56 NVVTMLIGRVDRMTTNLYLGMVSDLLILGLPDLVRLMRSRPMVGPILCRSL 115  
 Db 60 NLLTMLVSVSRRELRTTNLYLSSMAFSDLLIFLCPLDLVRLMQRPMNFGDLLCKLF 119  
 Qy 116 YVGECTVATLHMTALSVRYLAICRPLRVLVTRRRVRLAVLWAVALLSAGPFLF 175  
 Db 120 FVSECTVATVLTITLALSVRYFAICPLRAKVVTKGVKLVILVWAVAFCSAGPIFV 179  
 Qy 176 LVGVEQDFGISVWPLNGTARIASSPLASSPPLMLSRAPPSPGPPGTBAALFSPREC 235  
 Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197  
 Qy 236 RPS--PAQLGALRVMLWTATYAFPLCLSLYGLIGELWSSRRPLRGAASG---RE 290  
 Db 198 RATEFAVRSGLLTVMWVSSVFFFLPVFLVCLVSLYSLGRKLW--RR--RGAAVGSSLRD 253  
 Qy 291 RGHQTVRVLLVWVLAFTICWLPHFVGRIIYNTEDS---RMVFSQYFNVAIQLFVLS 347  
 Db 254 QNHKQTVKMLAVVFAFLCWLPFHVGRIYFSKSPGSLGSLAQISQYCNLSVFLVFL 313

QY 348 ASINPILYNLSKKYRAAFKLL 370  
Db 314 AAIPILYNLSKKYRAAFKLL 336

RESULT 8  
GHSR\_RAT  
ID\_GHSR\_RAT STANDARD; PRT; 364 AA.  
AC O08725;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor).  
GN Name=Ghsr;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary;  
RX MEDLINE=9724555; PubMed=902793; DOI=10.1210/me.11.4.415;  
RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P., Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;  
RT "Molecular analysis of rat pituitary and hypothalamic growth hormone secretagogue receptors.";  
RL Mol. Endocrinol. 11:415-423(1997).  
RN [2]  
RP SEQUENCE OF 1-240 FROM N.A.  
RC STRAIN=Wislat; TISSUE=Pituitary;  
RX MEDLINE=98100386; PubMed=9437732; DOI=10.1016/S0196-9781(97)00263-5;  
RA Yokote R., Sato M., Matsubara S., Ohye H., Niimi M., Murao K., Takahara J.;  
RT "Molecular cloning and gene expression of growth hormone-releasing peptide receptor in rat tissues.";  
RL Peptides 19:15-20(1998).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;  
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;  
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";  
RL Nature 402:656-660(1999).  
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6) as well as non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0677, adenosine) (by similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
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CC  
CC EMBL; U94321; AAC53156.1; -;  
CC RGD; AB001982; BAA31777.1; AUT\_INIT.  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm.1.1.  
CC PRINTS; PR00237; GPCRHO00PSN  
CC PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Glycoprotein; Transmembrane.  
FT DOMAIN 1 40 Extracellular (Potential).  
FT TRANSMEM 41 66 1 (Potential).  
FT DOMAIN 67 72 Cytoplasmic (Potential).  
FT TRANSMEM 73 96 2 (Potential).

QY 117 117 Extracellular (Potential).  
FT TRANSMEM 118 139 3 (Potential).  
FT DOMAIN 140 162 Cytoplasmic (Potential).  
FT TRANSMEM 163 183 4 (Potential).  
FT DOMAIN 184 211 Extracellular (Potential).  
FT TRANSMEM 212 235 5 (Potential).  
FT DOMAIN 236 263 Cytoplasmic (Potential).  
FT TRANSMEM 264 285 6 (Potential).  
FT DOMAIN 286 302 Extracellular (Potential).  
FT TRANSMEM 303 326 7 (Potential).  
FT DOMAIN 327 364 Cytoplasmic (Potential).  
FT DISULFID 115 197 By similarity.  
FT CARBOHYD 13 13 N-linked (GLCNAc...) (Potential).  
FT CARBOHYD 26 26 N-linked (GLCNAc...) (Potential).  
FT CARBOHYD 187 187 N-linked (GLCNAc...) (Potential).  
SQ SEQUENCE 364 AA; 40963 MW; DCBF559B061EE8 CRC64;

Query Match 40.0%; Score 861.5; DB 1; Length 364;  
Best Local Similarity 48.3%; Pred. No. 3.1e-49;  
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPPLGALVPVTAVCICLFLVGVSG 55  
Db 2 WNAI--PSEEPNPVTLDDWDASPGNDLPLFPAPLLAGVTATCVAFVVGISG 59  
QY 56 NVVTMLIGRYDRMTTNNLYGSMNVSDLLILGLPFDLYLRWSRPWFGPLLRLSL 115  
Db 60 NLATMLVVSFRPRELRTTNNLYSSMAFSDLLIFLCPLDLVRLWQYRPWNEFDLLCKLFQ 119  
QY 116 YVGECTYATLLHMTALSVRYLAICPLARVAVTRRRVPAALAVLWALLSNGPLP 175  
Db 120 FVSECTYATVLTITLALSRYFAICPLRAKVVTGRVKLVILVIMAWAFCSAGPIFV 179  
QY 176 LVGVEQDPGISVVPGLNGTARIASSPLASSPLWLSRAPSPSPGPETAEEAALFSREC 235  
Db 180 LVGYEHE-----NGT-----DPRD-----TNEC 197  
QY 236 RPS--PAQLGALRYMLVMTTAYFPFLPCLISILYGLIGRELWSSRRPLRGPAAG--RE 290  
Db 198 RATEFAVRSGLLTVMWVSVVFPFLPVFLCTLVLYSLIGRKLW--RR--RGDAVAGSLRD 253  
QY 291 RGHROTQVLLVVLVLAIIICWLPFHVGRIRIYINTEDS----RMVYFSQYFNVALQLFVLS 347  
Db 254 QNHKQTVMLAVVVFVAFILCWLPHVGRYLFSPGFEPSUEIAQISQCNLVSVFLVYLS 313  
QY 348 ASINPILYNLSKKYRAAFKLL 370  
Db 314 AAIPILYNLSKKYRAAFKLL 336

RESULT 9  
Q7ZT14  
ID Q7ZT14 PRELIMINARY; PRT; 347 AA.  
AC Q7ZT14;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Growth hormone secretagogue receptor type 1a.  
GN Name=Ghxr; Synonyms=Gharia;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OC NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=white leghorn; TISSUE=Kidney, and Pituitary;  
RX MEDLINE=22874039; PubMed=14511992; DOI=10.1016/S0016-6480(03)00247-8;  
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tashima N., Wakita M., Shimada K.;  
RT "Molecular characterization of chicken growth hormone secretagogue receptor gene.";  
RL Gen. Comp. Endocrinol. 134:198-202(2003).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AB05994; BAC76443.1; -.  
 DR EMBL; AB05995; BAC76444.1; -.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0016520; F: growth hormone-releasing hormone receptor a. . .; IEA.  
 DR GO; GO:0004872; F: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:00007186; P: G-protein coupled receptor protein signalin. . .; IEA.  
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:00007186; P: G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR003905; GHS1\_Receptor.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR01417; GHSRECEPTOR.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 347 AA; 39439 MW; 7A7543A9A94222F4 CRC64;  
 Query Match 39.7%; Score 855; DB 2; Length 347;  
 Best Local Similarity 47.0%; Pred. No. 7.9e-49;  
 Matches 165; Conservative 70; Mismatches 68; Indels 48; Gaps 6;  
 QY 33 FPLGALVPVAVCLCLFVVGVSGNVVTVMLIGRYDRMTTNNLYLGSMVSDLLILGLP 92  
 DB 19 FPAPVLGTGIVACVLLFVVGVGLNMLVWSRFRDMMTTFNLYSSMAFSDLLIFLCP 78  
 QY 93 FLYRLMRSRPVFGPLCRSLYGVGEGTATLHMTALSVERVLAICRLRLARVLVTR 152  
 DB 79 LDFRLMQVRPNWFGDLCKLPQFISESTVITLNTALSVERVLAICFLRLAKVIITK 138  
 QY 153 RVRRLAIWALVALLSAGPFLFVGVQDPGIVGVPLNGTARTASSPLASSPPLWLSR 212  
 DB 139 RKVKLVILWAVSFISAGPIFVLGVGHE-----NGT-----NPLSTN----- 177  
 QY 213 APPSPSPGPTAAEAALFSRECRPSAQL--GALRVMLVWTVTAYFFLPFLCLSLYLGI 270  
 DB 178 -----ECRATEVAIRSGLLTIWMISSIFFLPVFCVTLVYSLI 216  
 QY 271 GRELWSSRRPLGPAASGRGHRQTRVLLVVLVAFILCWLPHFVGRILYINTEDS--- 327  
 DB 217 GKRLWRKRNKTPSTIIRDKNKQTVKMLVVVVFALICWLPFHVGRYLFKSFEAGSL 276  
 QY 328 RMVFSQYFNIVALQFLYSASINPILYNLSKRYRAAFAKLLARKSRPR 378  
 DB 277 EIAVISQYCNLVSGFVLYLSAAINPILYNLSKRYRAACR-LFGLKALPK 326

## RESULT 10

O93412 PRELIMINARY; PRT; 374 AA.  
 AC O93412;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Orphan G protein-coupled receptor.  
 OS Spherooides nephelus  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Spherooides.  
 OX NCBI\_TaxID=391110;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20092336; PubMed=10628755; DOI=10.1210/me.14.1.160;  
 RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,  
 RA Gao Y.D., Schleich K.D., Yang L., Morriello G.J., Nargund R.,  
 RA Patchett A.A., Howard A.D., Smith R.G.;  
 RT "Ligand activation domain of human orphan growth hormone (GH)  
 RT secretagogue receptor (GHS-R) conserved from Pufferfish to humans."  
 RL Mol. Endocrinol. 14:160-169(2000).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

DR EMBL; AF082209; AAC33472.1; -.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0016520; F: growth hormone-releasing hormone receptor a. . .; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:00007186; P: G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR003905; GHS1\_Receptor.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR01417; GHSRECEPTOR.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 374 AA; 42324 MW; 2CF9304F004C7A16 CRC64;  
 Query Match 39.5%; Score 851; DB 2; Length 374;  
 Best Local Similarity 45.5%; Pred. No. 1.5e-48;  
 Matches 187; Conservative 65; Mismatches 101; Indels 58; Gaps 12;  
 QY 5 WNGS-DGEGAREPPWALPPCDERRCSPPFLGALVPVAVCLCLFVVGVSGNVTVMLI 63  
 DB 13 WEGHNHTAGLELPP-----LNYSIPLLAIVITVACTVLFVGVGVNMTILVV 61  
 QY 64 GRYDRMTTNNLYLGSMVSDLLILGLPFLDLYRLMRSRPVFGPLCRSLYGVGECTY 123  
 DB 62 SRYDRMTTNNLYLGSMVSDLLIFVCMPLDLYRMWRYRPRWFGDALCKLFQFVSECTY 121  
 QY 124 ATLLHMTALSVERVLAICRLRLARVLVTRRVRRLAIWALVALLSAGPFLFVGVQDP 183  
 DB 122 STILCITALSVERVLAICFLRLAKALVTKRVRRLAILLLMTVLSLSAGPVFVWGVSEKDS 181  
 QY 184 GISVVPGLNGTARTASSPL--ASSPPLMLSRAPPSPGPTAAEAALFSRECRPS--PA 240  
 DB 182 --IMFPN-----SSDLNESSWPL-----EAVDTRCMTQYAV 212  
 QY 241 QLGALRVMLVWTVTAYFFLPFLCLSLYLGILGRELWSSRRPLR-GPAASGRGHRQTRV 299  
 DB 213 ESGLMEAMVWLVSSVFFMPVFCVTLVYGLIGRLRLHRETTINSRVAYRDKSNRQTKM 272  
 QY 300 LNVVVLAFILCWLPHFVGRILYINTEDS---RMVFSQYFNIVALQFLYSASINPILYN 356  
 DB 273 LVVVVLAPVLCWLPHFVGRYLOFRLDAPSLLSLEYCSLVSVVLYLSAANPILYN 332  
 QY 357 LISKKYRAAFAKLLARKSRPRGFRSRDRTAGEVAGDTGSDTVGYTTSAN 407  
 DB 333 TMSWKYGAVALFVGVSDSPQ---RGR-TASTVKMD-----GWTESTVS 373

## RESULT 11

O93412 PRELIMINARY; PRT; 366 AA.  
 AC O93412;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Ghrelin/growth hormone secretagogue receptor.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pituitary gland;  
 RA Murata T., Ikegami R., Morita Y., Shinozaki K.;  
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY093948; AAM19733.1; -.  
 DR EMBL; AY093949; AAM19734.1; -.  
 DR EMBL; AY093950; AAM19735.1; -.  
 DR GO; GO:0016021; C: integral to membrane; IEA.



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DR GO:0007186; P-G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR; transmembrane.
KW G-protein coupled receptor; Receptor; transmembrane.
SQ SEQUENCE 295 AA; 33883 MW; E7397DCAEDF73873 CRC64;

Query Match
Best Local Similarity 31.1%; Score 671; DB 2; Length 295;
Matches 140; Conservative 43; Mismatches 72; Indels 54; Gaps 7;

QY 17 PWPALPPCDERRCS-----PPPLG-----ALVPVAVCLFVVGSGNV 57
DB 2 PWPNLSECLNSWEETRNRKFDLGLPLPNYISPLLTGTTIACLTLLFLVGAGNV 61
QY 58 VTVMLIGRYDRMTTNNLYGSMAYSDLLILGLPDLVRLWRSRPVFGPLLCRLSLV 117
DB 62 MTLVVKYRDMRTTNNLYGSMAYSDLLIFLCPDLVRLWRYRPFWDALCKLFQV 121
QY 118 GEGCTATLHMTALSVRYLAICPLRARVLVTRRRVRLAVLWAVALLSAGPFLV 177
DB 122 SESTVSTILSITALSVRYLAICPLRAKALVTRRRVRLAILLLWTVSLLSAGVFV 181
QY 178 GYEQD---PGISVPLNGTARIASPLSPPLWLSRAPPSPSGPETAAALFSRE 234
DB 182 GYERDSMFGNLSWGMNGTGF-----PEEGD-----TRE 212
QY 235 CRPS--PAQGLARVLMVLTAYFFLPFLCLSLYLGLIGRELWSSRRPLR-GPAASGR 291
DB 213 CKMTHYAVESGLMGAMVLSVFFFPVCLVLSLGRRLWQRHRETNINSRVAREK 272
QY 292 GHRQTVRL 300
DB 273 SNRQIKML 281

RESULT 14
Q72ZJ8 PRELIMINARY; PRT; 267 AA.
AC Q72ZJ8
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1b.
GN Name=Gharib;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY LOCATION: Integral membrane protein (by similarity).
DR EMBL; AB095997; BAC76446.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P-G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.

DR GO:0007186; P-G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL1_2; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR; transmembrane.
KW G-protein coupled receptor; Receptor; transmembrane.
SQ SEQUENCE 295 AA; 33883 MW; E7397DCAEDF73873 CRC64;

Query Match
Best Local Similarity 29.8%; Score 643; DB 2; Length 267;
Matches 124; Conservative 58; Mismatches 54; Indels 50; Gaps 5;

QY 33 PFLGALVEPTAVCLFVVGSGNVVTVMLIGRYDRMTTNNLYGSMAYSDLLILGLP 92
DB 19 PPAVLTGTVACVLLFVVGVLNMTLWVSFRDMRTTNNLYGSMAYSDLLIFLCP 78
QY 93 FDLVLRWSRPVFGPLLCRLSLVVGECCTATLHMTALSVRYLAICPLRARVLVTR 152
DB 79 LDLFRLQYRPNWFGDGLCKLFQFISSECTYSTINLTALSVRYLAICPLRARVIITK 138
QY 153 RRVRLATLWAVALLSAGPFLVVGVEQDPGISVPLNGTARIASPLSPPLWLSR 212
DB 139 RKVKLVILLWAVSFISAGPIFVLVGEHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSGPETAAALFSRECPSPAQL--GALRVMLWTVTAYFFLPFLCLSLYLGLI 270
DB 178 -----ECRATEYAIRSGLLTMMWISSIFFFLPVFCLVLSLI 216
QY 271 GRELWSSRRPLRGPAASGRERHQTIVRL-----LVVLAFLIIC 310
DB 217 GRKLWRRKRNIGSTIIRDKNNKQTVKMLGMAPRALCLQVRVLVC 262

RESULT 15
O93414 PRELIMINARY; PRT; 559 AA.
AC O93414
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spherooides nephelus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spherooides.
OX NCBI_TaxID=39110;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20092336; PubMed=10628755; DOI=10.1210/me.14.1.160;
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,
RA Patchett A.A., Howard A.D., Smith R.G.;
RT "Ligand activation domain of human orphan growth hormone (GH)
secretagogue receptor (GHS-R) conserved from Pufferfish to humans.";
RL Mol. Endocrinol. 14:160-169(2000).
DR EMBL; AF082211; AAC33474.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P-G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR; transmembrane.
KW Receptor.
SQ SEQUENCE 559 AA; 61956 MW; AFB9F35FAF0CD5F6 CRC64;

Query Match
Best Local Similarity 28.2%; Score 608; DB 2; Length 559;
Matches 156; Conservative 65; Mismatches 124; Indels 180; Gaps 12;

QY 22 LPDCDERRC---SPFLGALVPVTVAVCLFVVGSGNVVTVMLIGRYDRMTTNNLYG 78
DB 20 LHKCSNCEHWEFPV-FGMIVCVTIYIPLMLFGLNLTILVWLPYRMSSTLYLS 78

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QY 79 SNAVSDDLILLGLPDLRLRSRPPWVGPGLLCRLSLVVGECCTVATLLHMTALSVERYL 138
Db 79 SLAVSDIILLLLPVDLYKLRPREWPFGEIFCKSTMPFSECCTFCSILHITFISLERYL 138
QY 139 AICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVGVF---QDPGIS----- 186
Db 139 AVCWFTAKTVVTRRTTIICIWLGAAISAPVWVWGVVEVQSEDOGLSGWRESGAW 198
QY 187 -----VVVPG----- 191
Db 199 TGKEGEGFIIGERERENRDKGLKDEQLEEMNMWCKENNECGDKNGVTGFKGDKSLEV 258
QY 192 -NGTARIASSPPLASPPPLWLSRAPPPSPGPF-----TAERAAALFSRECRPS--PAQLGA 244
Db 259 CEGTKEQEHGERAAREGEAEQAQNKWKEDEGGGEGEDTDGGGRMQVDTRCRTCCTDYAVSSGL 318
QY 245 LRVMMLWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAAGRGRGHROTVRVLLVVV 304
Db 319 LSAMLVLSNMVFLVPLCILGLVIGLIGRTLM-----LRS-QISRRDVNNRNTVKNLGVIV 372
QY 305 LAFIICWLPFHVGRIIY-----INTE-----DSR----- 328
Db 373 LVFVLCWLPFHVGRITFFPSLGSDRPGVNASHALDLSRVPLELPPPGALGESDEAAGDAP 432
QY 329 ----- 328
Db 433 SEAQTGRDGGRAVLDTTRGTEARSDEGAAGPSTPEATTADPYDAENSTPLDDTHSHSQYF 492
QY 329 MMVFSQYFNIVALQLPYLSASINPILYNLISKKYRAAAFKLLAR 373
Db 493 LYXLSQYFNLVSSVLYLSAAINPLLYNLMSEYRYHVAHSLPRR 537
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Job time : 69.6015 secs

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:45:34 ; Search time 6014.47 Seconds  
(without alignments)  
11198.460 Million cell updates/sec

Title: US-09-719-485-4  
Perfect score: 1390  
Sequence: 1 atgggcagccctggaacgg.....acgtgaagacatgggataa 1390

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1390	100.0	1390	6	BD211244	BD211244 Cloning a
2	1161	83.5	1161	6	AX154591	AX154591 Sequence
3	1078	77.6	1239	6	BD211243	BD211243 Cloning a
4	1078	77.6	1239	6	CQ724376	CQ724376 Sequence
5	1078	77.6	1239	6	CQ831848	CQ831848 Sequence
6	1078	77.6	1239	6	AX154589	AX154589 Sequence
7	1078	77.6	1239	6	AX549187	AX549187 Sequence
8	1078	77.6	1239	6	AX572965	AX572965 Sequence
9	1078	77.6	1239	9	AV603964	AV603964 Homo sapi
10	1052	75.7	2040	9	AF034632	AF034632 Homo sapi
11	1052	75.7	163284	9	AL137000	AL137000 Human DNA
12	1052	75.7	341560	2	AL596304	AL596304 Homo sapi
13	1052	75.7	349980	6	AX711879	AX711879 Sequence
14	1052	75.7	349980	6	AX739961	AX739961 Sequence
15	1038	74.7	3066	6	BD211242	BD211242 Cloning a
16	900	64.7	900	6	BD211249	BD211249 Cloning a
17	592.2	42.6	692	9	HSA339407	AJ339407 Homo sapi
18	572.2	41.2	692	9	HSA342408	AJ342408 Homo sapi
19	557.4	40.1	615	9	HSA339459	AJ339459 Homo sapi

20	424.8	30.6	701	9	HSA326768	AJ326768 Homo sapi
21	338	24.3	602	6	BD211251	BD211251 Cloning a
22	307	22.1	191949	2	AC109158	AC109158 Mus muscu
23	283	20.4	283	6	AR168467	AR168467 Sequence
24	283	20.4	283	6	AR182284	AR182284 Sequence
25	283	20.4	283	6	AR303910	AR303910 Sequence
26	283	20.4	283	6	BD056681	BD056681 Galanin r
27	283	20.4	283	6	BD064652	BD064652 Human gal
28	283	20.4	283	6	BD064664	BD064664 Mouse gal
29	266.8	19.2	573	9	HSA341295	AJ341295 Homo sapi
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36	234.8	16.9	1063	6	AR156351	AR156351 Sequence
37	234.8	16.9	1101	4	SSU60178	U60178 Sus scrofa
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39	231.6	16.7	1095	6	BD221741	BD221741 Mouse gro
40	231.6	16.7	1095	6	AR454841	AR454841 Sequence
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42	231.6	16.7	4009	6	AR454840	AR454840 Sequence
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44	230	16.5	110000	2	AC095360_2	Continuation (3 of
45	230	16.5	183099	2	AC117349	AC117349 Rattus no

ALIGNMENTS

RESULT 1	BD211244	1390 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD211244	Cloning and identification of motilin receptor.			
DEFINITION	BD211244				
ACCESSION	BD211244.1	GI:33021014			
VERSION	JP 2002517507-A/3.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (Bases 1 to 1390)				
AUTHORS	Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macneil,D., Howard,A.D., Pong,S.S. and Smith,R.G.				
TITLE	Cloning and identification of motilin receptor				
JOURNAL	Patent: JP 2002517507-A 3 18-JUN-2002;				
COMMENT	MERCK AND CO INC				
	OS Homo sapiens (human)				
	PN JP 2002517507-A/3				
	PD 18-JUN-2002				
	PF 08-JUN-1999 JP 2000553444				
	PR 12-JUN-1998 US 60/089098				
	PI SCOTT D FEIGHNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI DOUGLAS MACNEIL,				
	PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH				
	PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC C12N15/00				
	CC Cloning and identification of motilin receptor. FH Key				
	Location/Qualifiers				
FT	source	1..1390			
FT	Location/Qualifiers	/organism='Homo sapiens (human)'			
FEATURES	source	1..1390			
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ORIGIN					
	Query Match	100.0%; Score 1390; DB 6; Length 1390;			
	Best Local Similarity	100.0%; Pred. No. 2.8e-175;			
	Matches 1390; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			







QY 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGACCGCGGCGG 840  
DB 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGACCGCGGCGG 840  
QY 841 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGAGCCACCGCAGACCGTCCGCGTCTG 900  
DB 841 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGAGCCACCGCAGACCGTCCGCGTCTG 900  
QY 901 CGTAAGTGGAGCGCGCGTGGTTCCAAAGACGCTGCTGCAGTCCGCGCCCGCGGGAGC 960  
DB 901 C----- 901  
QY 961 GCGCAACGCTGGGTCCCTTCCCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 1020  
DB 902 ----- 901  
QY 1021 TTTCTATTTCGATTCAGCTCCACCGCGTGGTGGTCTGGCATTTATAATTG 1080  
DB 902 -----TGGTGGTGGTCTGGCATTTATAATTG 929  
QY 1081 TGGTGGTGGTTCACGTTGGCAGATCATTTACATAAACACGGAAGATTCCGCGATGAT 1140  
DB 930 CTGGTGGCTTCCACGTTGGCAGATCATTTACATAAACACGGAAGATTCCGCGATGAT 989  
QY 1141 GTACTTCTCTAGTACTTTAAACATCGCTGCTGCAACTTTTCTATCTGAGCGCATCTAT 1200  
DB 990 GTACTTCTCTAGTACTTTAAACATCGCTGCTGCAACTTTTCTATCTGAGCGCATCTAT 1049  
QY 1201 CAACCAATCTCTACAACTCATTTCAAAGAGTACAGAGCGGCGGCTTTAACTGCT 1260  
DB 1050 CAACCAATCTCTACAACTCATTTCAAAGAGTACAGAGCGGCGGCTTTAACTGCT 1109  
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QY 1321 TGCAGGAGACACTGAGGAGACACCGTGGGCTACACCGAGACAAGCGCTAACGTGAAGAC 1380  
DB 1170 TGCAGGAGACACTGAGGAGACACCGTGGGCTACACCGAGACAAGCGCTAACGTGAAGAC 1229  
QY 1381 GATGGGATAA 1390  
DB 1230 GATGGGATAA 1239  
RESULT 5  
LOCUS CQ831648 1239 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 1 from Patent WO2004057328.  
ACCESSION CQ831648  
VERSION CQ831648.1 GI:50831561  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Golz,S., Bruggemeier,U. and Summer,H.  
TITLE Diagnostics and therapeutics for diseases associated with  
g-protein-coupled receptor 38 (gpr38)  
JOURNAL Patent: WO 2004057328-A 1 08-JUL-2004;  
Bayer HealthCare AG (DE)  
FEATURES  
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Query Match 77.6%; Score 1078; DB 6; Length 1239;  
Best Local Similarity 89.1%; Pred. No. 7.3e-134;  
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

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QY 61 GCGCTGCCGCGCTTCGAGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120  
DB 61 GCGCTGCCGCGCTTCGAGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120  
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DB 121 GTGACCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 181 ATGTGATTCGGGCGCTTACCGGAGCATGCGGACACCACTTGTATCTTGGGCAAGATG 240  
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QY 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGCTGCGACCTGCTACCGCTCTGGGCG 300  
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QY 301 TCGGCGCCCTGGGTGTTTCGGGCGCGTCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTG 360  
DB 301 TCGGCGCCCTGGGTGTTTCGGGCGCGTCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTG 360  
QY 361 TGCACCTACGCAACGCTGCTGCAATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420  
DB 361 TGCACCTACGCAACGCTGCTGCAATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420  
QY 421 TGGCGCGCGCTCCGCGCGCGGCTTGGTCAACCGGCGCGGCTCCGCGCGCTCATCGCT 480  
DB 421 TGGCGCGCGCTCCGCGCGCGGCTTGGTCAACCGGCGCGGCTCCGCGCGCTCATCGCT 480  
QY 481 GTGCTCTGGGCGCTGGGCGCTGCTCTGCTGCGCGCTCCCTTCTTGTCTGCTGGGCGCTCGAG 540  
DB 481 GTGCTCTGGGCGCTGGGCGCTGCTCTGCTGCGCGCTCCCTTCTTGTCTGCTGGGCGCTCGAG 540  
QY 541 CAGAACCCGCGCATCTCCGTAGTCCCGGCGCTCAATGGCACCGCGCGGATCGCCTCTCG 600  
DB 541 CAGAACCCGCGCATCTCCGTAGTCCCGGCGCTCAATGGCACCGCGCGGATCGCCTCTCG 600  
QY 601 CCTCTCGCTCTGCTGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
DB 601 CCTCTCGCTCTGCTGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
QY 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTCAAGCGCGCAATCGCGCGCGAGCCCGCGG 720  
DB 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTCAAGCGCGCAATCGCGCGCGAGCCCGCGG 720  
QY 721 CAGCTGGGCGCGCTGCGGTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB 721 CAGCTGGGCGCGCTGCGGTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
QY 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCGG 840  
DB 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCGG 840  
QY 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCCACCGGCGAGACCGTCCGCGTCTG 900  
DB 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGAGCCACCGGCGAGACCGTCCGCGTCTG 900  
QY 901 CGTAAGTGGAGCGCGCGTGGTTCCAAAGACGCTGCTGCAGTCCGCGCCCGCGGGAGC 960  
DB 901 C----- 901  
QY 961 GCGCAACGCTGGGTCCCTTCCCTGCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 1020  
DB 902 ----- 901  
QY 1021 TTTCTATTTCGATTCAGCTCCACCGCGTGGTGGTCTGGCATTTATAATTG 1080  
DB 902 -----TGGTGGTGGTCTGGCATTTATAATTG 929  
QY 1081 CTGGTGGCTTCCAGCTTGGCAGATCATTTACATAAACACGGAAGATTCCGCGATGAT 1140



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RESULT 8  
AX572965  
LOCUS  
DEFINITION





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ORIGIN					
Query Match 77.6%; Score 1078; DB 9; Length 1239;					
Best Local Similarity 89.1%; Pred. No. 7.3e-134;					
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;					
Qy	1	ATGGGAGCCCTTGGAAACGCGACGACGCGCCCGAGGGGGCGCGGAGCCGCGTGGGCC	60		
Db	1	ATGGGAGCCCTTGGAAACGCGACGACGCGCCCGAGGGGGCGCGGAGCCGCGTGGGCC	60		
Qy	61	GGCTGGCGCTTGGAGAGCGCGCTGTCTCGCCCTTTCCCTTGGGGCGCTGTGTGCGG	120		
Db	61	GGCTGGCGCTTGGAGAGCGCGCTGTCTCGCCCTTTCCCTTGGGGCGCTGTGTGCGG	120		
Qy	121	GTGACCGCTGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	180		
Db	121	GTGACCGCTGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	180		
Qy	181	ATGCTGATCGGCGCTTACCGGACATCGGACACCACTGTCTGTCTGTCTGTCTGTCT	240		
Db	181	ATGCTGATCGGCGCTTACCGGACATCGGACACCACTGTCTGTCTGTCTGTCTGTCT	240		
Qy	241	GGCTGTCCGACTACTCATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	300		
Db	241	GGCTGTCCGACTACTCATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	300		
Qy	301	TGCGGGCGCTGGGTGTGGGGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	360		
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Qy	361	TGCACCTAGCCACGCTGTGCACATGACCGGCTCAGCTCGAGCGCTACCTGGCCATC	420		
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Qy	421	TGCGCGCGCTCCGCGCGCGCTTGTGTACCGCGCGCGCTCGCGCGCTCATCGCT	480		
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Qy	481	GTGCTGTGGCGCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	540		
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Qy	541	CAGGACCCGCGATCCGCTAGTCCGCGGCTCAATGGACCGCGCGGATCGCTCTCTCG	600		
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Qy	601	CCTCTCGCTGTCTCGCGCGCTTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	660		
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Qy	661	GGGCGCGAGACCGCGAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720		
Db	661	GGGCGCGAGACCGCGAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720		
Qy	721	CAGCTGGGGCGCTGGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780		
Db	721	CAGCTGGGGCGCTGGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780		

781	CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCG	84	
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Qy	841	CTGCGAGGCGCGCGCGCTTGGGGCGGAGAGAGCCACCGCAGACCGTCCGCGTCTG	900
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Qy	901	CGTAAGTGGAGCGCGTGTTCAAAGACGCTGCTCAGTCCGCCCGCGCGCGGAC	960
Db	901	CGTAAGTGGAGCGCGTGTTCAAAGACGCTGCTCAGTCCGCCCGCGCGCGGAC	960
Qy	961	GGCAAAACGCTGGTGGTCCCTTCCCTGTCTGCCAGCTCTGGGCGCGCTTCCAGCTCC	102
Db	902	-----	901
Qy	1021	TTTCCATTTCGATTCAGCTCCAGCTCCACCCCGCGTGTGTGGTCTTGGCAATTTAT	108
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Qy	1081	CTGGTTGCCCTTCCAGCTTGGCAGATCATTTACATAAAACGGAAGATTCGCGGATG	114
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Qy	1141	GTACTTCTCTCAGTACTTTAAACATCGTCTCTGCAACTTTTCTATCTGAGCGCATCT	120
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Qy	1201	CAACCAATCTCTTACAACCTCATTTCAAAGATACAGAGCGCGGCTTTAAACTGCT	126
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Qy	1321	TGCGGGGACACTGGAGGAGACACGCTGGGCTACACCGAGACGCTTAACGCTGAAGAC	138
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AF034632			
LOCUS			
DEFINITION			
Homo sapiens orphan G protein-coupled receptor (GPR38) gene,			
complete cds.			
ACCESSION			
AF034632			
VERSION			
AF034632.1 GI:2654158			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE			
1 (bases 1 to 2040)			
McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,			
Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,L.H.			
Cloning and characterization of two human G protein-coupled			
receptor genes (GPR38 and GPR39) related to the growth hormone			
secretagogue and neurotensin receptors			
Genomics 46 (3), 426-434 (1997)			
MEDLINE			
98110578			
PUBMED			
9441746			
REFERENCE			
2 (bases 1 to 2040)			
McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,			
Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.			
Direct Submission			
Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.			
Inc., PO Box 2000, Rahway, NJ 07065, USA			
LOCATION/Qualifiers			
FEATURES			

Qy	781	CTGTGCTCAGATCCTCTACGGGCTCATCGGGGGAGAGCTGTGTGAGCAGCCGCGGCGG	840
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Qy	1081	CTGTGTCCTTCCACGTTGGCAGATCATTTACATAAACGGAAGATTTCGCGGATGAT	1140
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Qy	1141	GTACTTCTCAGTACTTTAAACATCGTCTGTCAACTTTTCTATCTGAGCGCATCTAT	1200
Db	990	GTACTTCTCAGTACTTTAAACATCGTCTGTCAACTTTTCTATCTGAGCGCATCTAT	1049
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Qy	1261	GCTCGAAGAGTCCAGCGGAGAGGCTTCCACAGAGAGGAGACCTCGGGGGAAGT	1320
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RESULT 10			
AF034632			
LOCUS			
DEFINITION Homo sapiens orphan G protein-coupled receptor (GPR38) gene,			
complete cds.			
ACCESSION AF034632			
VERSION AF034632.1			
KEYWORDS GI:2654158			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
REFERENCE 1 (bases 1 to 2040)			
AUTHORS McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,			
Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,L.H.			
Cloning and characterization of two human G protein-coupled			
receptor genes (GPR38 and GPR39) related to the growth hormone			
secretagogue and neurotensin receptors			
Genomics 46 (3), 426-434 (1997)			
JOURNAL MEDLINE 98110578			
PUBMED 9441746			
REFERENCE 2 (bases 1 to 2040)			
AUTHORS McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,			
Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.			
Direct Submission			
TITLE Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,			
JOURNAL Inc., PO Box 2000, Rahway, NJ 07065, USA			
FEATURES Location/Qualifiers			

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2	ATGGGACGCTCTGAAAGCGACGACGCGCCCGGAGGGGGCGGAGCGCCGCGGCCC	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
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4	GGGCTGCGGCTCTGCGAGCGCGCTGCTGCGCCCTTTCCCTCGGGGCGCTGCTGCGG	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
5	GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
6	GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
7	ATGCTGATCGGCGCTACCGGACATCGGACACCACTTCTACTGCGGACGATG	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
8	ATGCTGATCGGCGCTACCGGACATCGGACACCACTTCTACTGCGGACGATG	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
9	GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGCTTCCGACCTGTACCGCTCTGCGGC	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
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11	TGCGGCGCTTGGGTGTTGGGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
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13	TGCACTAGCCACCTGCTGACATGACCGGCTCAGCGTACGAGCTACCTGCGCATC	660 660 720 720 780 780 840 840 900 900 960 960 1020 1020
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The true left end of clone RP11-452110 is at 1 in this sequence.  
 The true right end of clone RP11-103018 is at 163284 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-203116 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
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## FEATURES

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VERSION	AX711879.1 GI:29787684					
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ORGANISM	Homo sapiens					
REFERENCE						
AUTHORS	Zhang, Y., Moffatt, M., Cookson, W. and Tinsley, J.O.					
TITLE	Atopy					
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 11, 2005, 13:13:41 ; Search time 62.3985 Seconds  
(without alignments)  
3167.746 Million cell updates/sec

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Perfect score: 2043  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	674	33.0	295	2 Q6YGZ2	Q6YGZ2 acanthopagr
3	673.5	33.0	363	2 O93413	O93413 spherooides
4	671	32.8	385	2 Q6YDZ3	Q6YDZ3 acanthopagr
5	643	31.5	267	2 Q7ZZJ8	Q7ZZJ8 gallus gall
6	643	31.5	331	2 Q7ZZJ9	Q7ZZJ9 gallus gall
7	643	31.5	366	1 GHSR_HUMAN	Q92847 homo sapien
8	642.5	31.4	360	2 Q6B7N9	Q6B7N9 macaca fasc
9	641.5	31.4	374	2 O93412	O93412 spherooides
10	641	31.4	347	2 Q7ZT14	Q7ZT14 gallus gall
11	641	31.4	364	1 GHSR_MOUSE	O99P50 mus musculu
12	641	31.4	364	1 GHSR_RAT	O08725 rattus norv
13	641	31.4	366	1 GHSR_PIG	Q95254 sus scrofa
14	607	29.7	366	2 Q8MHZ5	Q8MHZ5 ovis aries
15	444	21.7	215	2 Q711Q7	Q711Q7 gallus gall
16	442	21.6	211	2 Q711Q8	Q711Q8 gallus gall
17	435	21.3	559	2 O93414	O93414 spherooides
18	376	18.4	123	2 Q80UB2	Q80UB2 mus musculu
19	356.5	17.4	426	2 Q8NE20	Q8NE20 homo sapien
20	354.5	17.4	403	2 Q7LDP6	Q7LDP6 homo sapien
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22	343	16.8	424	1 NTR1_RAT	P20789 rattus norv
23	340	16.6	424	1 NTR1_MOUSE	O89319 mus musculu
24	339	16.6	145	2 Q97914	Q97914 ovis aries
25	338	16.5	395	2 Q91Z76	Q91Z76 mus musculu
26	338	16.5	395	2 Q8BZ39	Q8BZ39 mus musculu
27	336	16.4	415	2 Q96AM5	Q96AM5 homo sapien
28	335	16.4	412	2 Q7LC54	Q7LC54 homo sapien
29	335	16.4	415	2 Q9GZQ4	Q9GZQ4 homo sapien
30	331.5	16.2	405	2 O55040	O55040 mus musculu
31	330	16.2	418	1 NTR1_HUMAN	P30989 homo sapien

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35	324.5	15.9	309	2 Q7QEG8	Q7QEG8 anopheles g
36	316	15.5	556	1 CAPR_DROME	Q81TC7 drosophila
37	311.5	15.2	413	2 Q65Y5A	Q65Y5A bombyx mori
38	309	15.1	428	2 Q9VFNA	Q9VFNA drosophila
39	309	15.1	430	2 Q8ITC9	Q8ITC9 drosophila
40	308	15.1	453	2 Q7KSK4	Q7KSK4 drosophila
41	308	15.1	295	2 Q7PDF2	Q7PDF2 anopheles g
42	307	15.0	340	2 Q7QBC1	Q7QBC1 anopheles g
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ALIGNMENTS

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DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Motilin receptor (G protein-coupled receptor 38).  
GN Name=MLNR; Synonyms=GPR38, MTLR, MTLRL1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;  
RT "Cloning and characterization of two human G protein-coupled receptor  
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RL Genomics 46:426-434 (1997).  
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RA O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,  
RA Howard A.D.;  
RT "Receptor for motilin identified in the human gastrointestinal  
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RL Science 284:2184-2188 (1999).  
RN [3]  
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RX PubMed=15057823; DOI=10.1038/nature02379;  
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 RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,  
 RT "The DNA sequence and analysis of human chromosome 13.",  
 RL Nature 428:522-528(2004).  
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 RX MEDLINE=21219832; PubMed=11322507; DOI=10.1395/ENDO.14.1.009;  
 RA Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,  
 RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.,  
 RT "Growth hormone secretagogue receptor family members and ligands.",  
 RL Endocrine 14:9-14(2001).  
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 CC Name=A;  
 CC IsoId=O43193-1; Sequences=Displayed;  
 CC Name=B;  
 CC IsoId=O43193-2; Sequences=VSP\_001894;  
 CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone  
 CC marrow.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
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 CC EMBL; AL137000; CAC19107.1; -;  
 CC Genew; HGNC:4495; MLNR.  
 CC MIM; 602885; -;  
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 CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
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 Transmembrane.  
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 FT TRANSMEM 36 56 1 (Potential).  
 FT DOMAIN 57 74 Cytoplasmic (Potential).  
 FT TRANSMEM 75 94 2 (Potential).  
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 FT (in isoform B).  
 FT /FTid=VSP\_001894.  
 SQ SEQUENCE 412 AA; 45344 MW; C13FF6165012DEF3 CRC64;  
 Query Match 77.4%; Score 1581; DB 1; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-99;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGSPWNSDGGEGAREPWPALPCDDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60  
 DB 1 MGSPWNSDGGEGAREPWPALPCDDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60  
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
 DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVERVLAICRPLRARVLVTRRRVRLIAVMAVALLSAGFFFLVGVE 180  
 DB 121 CTYATLLHMTALSVERVLAICRPLRARVLVTRRRVRLIAVMAVALLSAGFFFLVGVE 180  
 QY 181 QDRGISVVGNGTARTASSPLASPPPLWLSRAPPPSPSPETAEEAALFSRRCPSPA 240  
 DB 181 QDRGISVVGNGTARTASSPLASPPPLWLSRAPPPSPSPETAEEAALFSRRCPSPA 240  
 QY 241 QLGLRVLVMTVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHQRVRL 300  
 DB 241 QLGLRVLVMTVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHQRVRL 300  
 RESULT 2  
 Q6YGVZ2 PRELIMINARY; PRT; 295 AA.  
 ID Q6YGVZ2  
 AC Q6YGVZ2  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Growth hormone secretagogue receptor 1b.  
 OS Acanthopagrus schlegelii (Black porgy).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 CC Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes; Percoidae;  
 CC Sparidae; Acanthopagrus.  
 CC NCBI TaxID=72011;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;  
 RA Chan C.B., Cheng C.H.K.;  
 RT "Identification and functional characterization of two alternatively  
 RT spliced growth hormone secretagogue receptor transcripts from the  
 RT pituitary of black seabream Acanthopagrus schlegelii.",  
 RL Mol. Cell. Endocrinol. 214:81-95(2004).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC EMBL; AY151041; AAN7876.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR003905; GHS1\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR01417; GHSRECEPTOR.  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 295 AA; 33883 MW; E7397DCABDF73873 CRC64;  
 Query Match 33.0%; Score 674; DB 2; Length 295;  
 Best Local Similarity 45.3%; Pred. No. 3.9e-38;  
 Matches 141; Conservative 43; Mismatches 73; Indels 54; Gaps 7;

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QY 17 PPWALPPCDERRCS-----PPFLG-----ALVPVAVCLCLFVVGVSQNV 57
DB 2 PSWPNLSECLSNCSWEETRNRATKFDLGLPLNTYISPLLTGTITACTLLFLVGVAGNV 61
QY 58 VTMVLIGRYDRMTTNNLYLGSMAVSDLLILGLPDLRYLWRSRPWVFGPLLCRLSLYV 117
DB 62 MTLVSVKYRDMRTTNNLYLGSMAVSDLLILGLPDLRYLWRSRPWVFGPLLCRLSLYV 121
QY 118 GEGTYATLLHMTALSVRYLAICRPLARVLVTRRRVRLATVAVALLSAGPFLFLV 177
DB 122 SESCYSYLSLTALSVRYLAICRPLAKALVTRRRVRLATVAVALLSAGPFLFLV 181
QY 178 GVEOD---PGISVPLNGLTARIASSPLASSPPLWLSRAPPSPPSGPETAFAALFSRE 234
DB 182 GVERDSMPGNLSWVGNGTGF-----PEEGD-----TRE 212
QY 235 CRPS--PAQLGRLVMLAVTTAYFPLPFLCLSLYGLIGRELWSSRRPLR-GPAASGRER 291
DB 213 CMHTYAVESGLMAGVWLLSSVFFMPVFCULTVLYSLIGRLWQRHRETNINSRVAREK 272
QY 292 GHROTVRVLRK 302
DB 273 SNRQIKMLGK 283

RESULT 3
ID O93413 PRELIMINARY; PRT; 363 AA.
AC O93413;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spheroidea nephelus
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spheroidea.
NCBI_TaxID=39110;
RX SEQUENCE FROM N.A.
RP MEDLINE=2092336; PubMed=10628755; DOI=10.1210/me.14.1.150;
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,
RA Patchett A.A., Howard A.D., Smith R.G.;
RT "Ligand activation domain of human orphan growth hormone (GH)
RT secretagogue receptor (GHS-R) conserved from Pufferfish to humans.";
RL Mol. Endocrinol. 14:160-169(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF082210; AAC33473.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 363 AA; 41324 MW; 74518BD9CD310991 CRC64;

Query Match 33.0%; Score 673.5; DB 2; Length 363;
Best Local Similarity 49.6%; Pred. No. 5.2e-38;
Matches 135; Conservative 39; Mismatches 55; Indels 43; Gaps 4;

QY 31 SPFGALVPVAVCLCLFVVGVSQNVVTVMLIGRYDRMTTNNLYLGSMAVSDLLILGL 90

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DB 31 SLFPASTLIPVTVICILIFVVGVTGNTWTLLIQFKDMKTTTNNLYLSSMAVSDLVIFLC 90
QY 91 LPFDLYLRWRSRPWVFGPLLCRLSLYVGEGETYATLLHMTALSVRYLAICRPLARVLV 150
DB 91 LPFDLYLRWRSRPWVFGPLLCRLSLYVGEGETYATLLHMTALSVRYLAICRPLARVLV 150
QY 151 TRRRVRLATVAVALLSAGPFLFLVGVGEQDPGISVPLNGLTARIASSPLASSPPLW 210
DB 151 TRRRVQVITLALWCFALVSAAPTFLVGVVEYD-----NET----- 185
QY 211 SRAPPPSPGPETAFAALFSRCPSPAPL--GALRVMLVTTTAYFPLPFLCLSLYV 268
DB 186 ----HPDNTG-----QCKHTGYAISGQLHIMVWSTTYFFCPMLCLFLYV 229
QY 269 LIGRELWSSRRPLRGPASGRERGHROTVRV 300
DB 230 SIGCKLWKSNDLQGPCALARESHROTIVKIL 261

RESULT 4
QY Q6YGZ3 PRELIMINARY; PRT; 385 AA.
AC Q6YGZ3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Growth hormone secretagogue receptor 1a.
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
NCBI_TaxID=72011;
RX SEQUENCE FROM N.A.
RP PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;
RA Chan C.B., Cheng C.H.K.;
RT "Identification and functional characterization of two alternatively
RT spliced growth hormone secretagogue receptor transcripts from the
RT pituitary of black seabream Acanthopagrus schlegelii.";
RL Mol. Cell. Endocrinol. 214:81-95(2004).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY151040; AAN7875.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 385 AA; 43697 MW; 665CBDA9702887A9 CRC64;

Query Match 32.8%; Score 671; DB 2; Length 385;
Best Local Similarity 45.3%; Pred. No. 8.1e-38;
Matches 140; Conservative 43; Mismatches 72; Indels 54; Gaps 7;

QY 17 PPWALPPCDERRCS-----PPFLG-----ALVPVAVCLCLFVVGVSQNV 57
DB 2 PSWPNLSECLSNCSWEETRNRATKFDLGLPLNTYISPLLTGTITACTLLFLVGVAGNV 61
QY 58 VTMVLIGRYDRMTTNNLYLGSMAVSDLLILGLPDLRYLWRSRPWVFGPLLCRLSLYV 117
DB 62 MTLVSVKYRDMRTTNNLYLGSMAVSDLLILGLPDLRYLWRSRPWVFGPLLCRLSLYV 121
QY 118 GEGTYATLLHMTALSVRYLAICRPLARVLVTRRRVRLATVAVALLSAGPFLFLV 177
DB 122 SESCYSYLSLTALSVRYLAICRPLAKALVTRRRVRLATVAVALLSAGPFLFLV 181
QY 178 GVEOD---PGISVPLNGLTARIASSPLASSPPLWLSRAPPSPPSGPETAFAALFSRE 234
DB 182 GVERDSMPGNLSWVGNGTGF-----PEEGD-----TRE 212
QY 235 CRPS--PAQLGRLVMLAVTTAYFPLPFLCLSLYGLIGRELWSSRRPLR-GPAASGRER 291
DB 213 CMHTYAVESGLMAGVWLLSSVFFMPVFCULTVLYSLIGRLWQRHRETNINSRVAREK 272
QY 292 GHROTVRVLRK 302
DB 273 SNRQIKMLGK 283

Query Match 33.0%; Score 673.5; DB 2; Length 363;
Best Local Similarity 49.6%; Pred. No. 5.2e-38;
Matches 135; Conservative 39; Mismatches 55; Indels 43; Gaps 4;

QY 31 SPFGALVPVAVCLCLFVVGVSQNVVTVMLIGRYDRMTTNNLYLGSMAVSDLLILGL 90

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Db 122 SESCTYSTILSTALSVRYLAICFPLAKALVTKRRVRLALLLWTVLSSLSAGPVFMV 181
QY 178 GVEQD---PGISVWFLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRE 234
Db 182 GVERDSWPNGLSWGNGTGFF-----PEEGD-----TRE 212
QY 235 CPSP--PAQLGALRVMLVTTAYFELPFLCLSLYGLIGRELWSSRRPLR-GPAASGRER 291
Db 213 CQWTHAYVESGLMGAMVLLSSVFFPMPVFCUTLVLSLIGRLWQRHRTNINSRVAREK 272
QY 292 GHRQTVRVL 300
Db 273 SNRQIKWL 281

RESULT 5
Q7ZZJ8 PRELIMINARY; PRT; 267 AA.
AC Q7ZZJ8;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1b.
GN Name=Gharib;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB095997; BAC76446.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 267 AA; 30209 MW; 00563690B35AD107 CRC64;

Query Match 31.5%; Score 643; DB 2; Length 267;
Best Local Similarity 44.4%; Pred. No. 4.6e-36;
Matches 126; Conservative 54; Mismatches 56; Indels 48; Gaps 5;

QY 33 PFLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLILGLP 92
Db 19 FPAPVLGTITVACVLLFVVGVLGNLMTLVVSRFRDMRTTNLYLSSMAFSDLLIFLCP 78
QY 93 FDLVRLWRSRPPWFGPFLCLRLSLYVGECCTATLHMTALSVERYLAICRPLARVLVTR 152
Db 79 LDFRLWQYRPWNFGDLCKLKFQFISECTYSTILNITALSVERYVAICFPLRAKVIITK 138
QY 153 RRVRLAIWALVALLSAGPFLFLVGVEODPGISVVPGNGTARIASSPLASSPPLWLSR 212
Db 139 RKVKLVILLWAVSFISAGPIFLVGVEHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSPGPTAEAAALFSRECRPSAQL--GALRVMLWVTTAYFELPFLCLSLYGLI 270
Db 178 -----ECRATEYAIRSGLLTIMVWISSIFFFLPVFCLTVLSLI 216
QY 271 GRELWSSRRPLRGPAAASGRGRHQTQTVRLRKW 303
Db 217 GRKLWRRKRNKGNPSTIIRDKNKNQTVKMLGRY 249

RESULT 7
GHSR_HUMAN
ID GHSR_HUMAN STANDARD; PRT; 366 AA.

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Db 217 GRKLWRRKRNKGNPSTIIRDKNKNQTVKMLGRAPRA-----LCLQ 256

RESULT 6
Q7ZZJ9 PRELIMINARY; PRT; 331 AA.
AC Q7ZZJ9;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1a variant.
GN Name=Gherlav;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsushima N.,
RA Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
receptor gene.";
RL Gen. Comp. Endocrinol. 134:198-202(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB095996; BAC76445.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 331 AA; 37567 MW; 1BE477BF2D7A3BEB CRC64;

Query Match 31.5%; Score 643; DB 2; Length 331;
Best Local Similarity 44.7%; Pred. No. 5.6e-36;
Matches 122; Conservative 56; Mismatches 51; Indels 44; Gaps 4;

QY 33 PFLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLILGLP 92
Db 19 FPAPVLGTITVACVLLFVVGVLGNLMTLVVSRFRDMRTTNLYLSSMAFSDLLIFLCP 78
QY 93 FDLVRLWRSRPPWFGPFLCLRLSLYVGECCTATLHMTALSVERYLAICRPLARVLVTR 152
Db 79 LDFRLWQYRPWNFGDLCKLKFQFISECTYSTILNITALSVERYVAICFPLRAKVIITK 138
QY 153 RRVRLAIWALVALLSAGPFLFLVGVEODPGISVVPGNGTARIASSPLASSPPLWLSR 212
Db 139 RKVKLVILLWAVSFISAGPIFLVGVEHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSPGPTAEAAALFSRECRPSAQL--GALRVMLWVTTAYFELPFLCLSLYGLI 270
Db 178 -----ECRATEYAIRSGLLTIMVWISSIFFFLPVFCLTVLSLI 216
QY 271 GRELWSSRRPLRGPAAASGRGRHQTQTVRLRKW 303
Db 217 GRKLWRRKRNKGNPSTIIRDKNKNQTVKMLGRY 249

RESULT 7
GHSR_HUMAN
ID GHSR_HUMAN STANDARD; PRT; 366 AA.

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Spheroideae.  
 OK NCBI\_TaxID=39110;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20092336; PubMed=10628755; DOI=10.1210/me.14.1.160;  
 RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,  
 RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,  
 RA Patchett A.A., Howard A.D., Smith R.G.,  
 RT "Ligand activation domain of human orphan growth hormone (GH)  
 RT secretagogue receptor (GHS-R) conserved from Pufferfish to humans."  
 RL Mol. Endocrinol. 14:160-169(2000).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AF082209; AAC33472.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR003905; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR01417; GHSRECEPTOR.  
 DR PROSITE; PS00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL\_2; 1.  
 DR InterPro; IPR003905; GPCR\_Rhodopsn.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 374 AA; 42324 MW; 2CF9304F004C7A16 CRC64;  
 Query Match 31.4%; Score 641.5; DB 2; Length 374;  
 Best Local Similarity 45.8%; Pred. No. 8e-36;  
 Matches 138; Conservative 45; Mismatches 73; Indels 45; Gaps 8;  
 QY 5 WNGS-DGEGAREPPWALPPCDERRCSPPPLGALVPVAVCLCLFVVGVSNGVVTMLI 63  
 DB 13 WEGSHNGTAGLEPP-----LNYSIPLAVITVACTVLTFTVGVGVNMTILV 61  
 QY 64 GRYDMRTTNYLGSMAVSDLLILGLPDLYLWRSPWVFGPLLCRLSLYVGEGCTY 123  
 DB 62 SYRDMRTTNYLGSMAVSDLIFVCMPLDLYRMWYRPFWDGALCKLFQFVSECTY 121  
 QY 124 ATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGEQDP 183  
 DB 122 STLCITALSVERYLAI CFLRAKALVTKRRVALILLWTVLSLSAGPFWVGVGVKDS 181  
 QY 184 GISVVPGLNGTARTIASPL-ASSPPLWLSRAPPPSPGPETAALFSECRPS--PA 240  
 DB 182 --IMPN-----SSDLNESSWPL-----EAYDTECRMTQYAV 212  
 QY 241 QLGLARVLMVLTAYFFLPFLCLSLYGLIGRELWSSRRPLR-GPAASGRGRGHRTVVR 299  
 DB 213 ESGLMEAMVWLSSVFFFPVFLVTLVLYGLIGRLRLRHRETINSRVAYRDKSNQTIKM 272  
 QY 300 L 300  
 DB 273 L 273  
 RESULT 10  
 Q7ZT14  
 ID Q7ZT14 PRELIMINARY; PRT; 347 AA.  
 AC Q7ZT14;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Growth hormone secretagogue receptor type 1a.  
 GN Name=Ghar; Synonyms=Ghsrla;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Spheroideae.  
 OK NCBI\_TaxID=9541;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX Hellings S.E. III.;  
 RT "Macaca fascicularis growth hormone secretagogue receptor cloning";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY675630; RA77421.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR003905; GPCR\_Rhodopsn.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR01417; GHSRECEPTOR.  
 DR PROSITE; PS00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL\_2; 1.  
 DR InterPro; IPR003905; GPCR\_Rhodopsn.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON TER 1  
 SQ SEQUENCE 360 AA; 40699 MW; DAC4AC726EE9468E CRC64;  
 Query Match 31.4%; Score 642.5; DB 2; Length 360;  
 Best Local Similarity 47.4%; Pred. No. 6.6e-36;  
 Matches 136; Conservative 40; Mismatches 64; Indels 47; Gaps 6;  
 QY 19 WPAIPCD---ERRCSPPFLGALVPVAVCLCLFVVGVSNGVVTMLIGRYDMRTTTL 75  
 DB 15 WPAIPCD---ERRCSPPFLGALVPVAVCLCLFVVGVSNGVVTMLIGRYDMRTTTL 74  
 QY 76 YLGSMAVSDLLILGLPDLYLWRSPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVE 135  
 DB 75 YLGSMAVSDLLILGLPDLYLWRSPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVE 134  
 QY 136 RYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGEQDPGISVVPGLNGTA 195  
 DB 135 RYFAICFPLRAKVVVTKGRVGLIIFVIAVAFCSAGPIFLVGVGEH-----NGT- 184  
 QY 196 RIASSPLASSPPLWLSRAPPPSPGPETAALFSECRPS--PAQLGALRVMLWVT 253  
 DB 185 -----DP--W-----DTNECRTEFAVRSGLTIVWVSS 212  
 QY 254 AYFFLPFLCLSLYGLIGRELWSSRRPLRGPASGRGRGHRTVVRVL 300  
 DB 213 IFFFLPVFCLTVLYSLIGRLWRRRGDAVVGASLRDQNHQKQTKML 259  
 RESULT 9  
 O93412  
 ID O93412 PRELIMINARY; PRT; 374 AA.  
 AC O93412;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Orphan G protein-coupled receptor.  
 OS Spheroideae nephelus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





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FT DOMAIN 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT DOMAIN 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT DOMAIN 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT DOMAIN 327 364 Cytoplasmic (Potential).
FT DISULFID 115 197 By similarity.
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).
FT CONFLICT 59 59 G -> S (in Ref. 2).
SQ SEQUENCE 364 AA; 40963 MW; 8F1214E585F3B2E8 CRC64;

Query Match 31.4%; Score 641; DB 1; Length 364;
Best Local Similarity 45.8%; Pred. No. 8.5e-36;
Matches 142; Conservative 41; Mismatches 65; Indels 62; Gaps 10;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGSG 55
Db 2 WNAT--PSEEPENVTLDLDWDASFGNDSLPDELPLFPAPLAGVTATCVATFVVGISG 59

QY 56 NVVTMLIGRYDMRTTNLYLGSMVAVSDLLILGLPFDLYLWRSRPPWFGPLLCRLSL 115
Db 60 NLLTMLVSRFRRLRTTNLYLSSMAFSDLLIFLCPLDLVLMQYRPNWFGDLLCKLFQ 119

QY 116 YVGECTYATLHMTALSVERYLACRPLRVLVTRRRVRLALAVLWALLSAGPFLF 175
Db 120 FVSECTYATVLTITALSVERYFAICFLPRAKVVTKGRKVLVILVAVAFCSAGPIFV 179

QY 176 LVGVQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSREC 235
Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQIGALVRLMVTYVTFPLCLSLYLGIGELWSSRRPLRGPAAAG---RE 290
Db 198 RATEFAVRSGLLTVNVMVSSVFFFLVFLVCLTVLYSLIGKLV--RR--RGDAAGVSSLD 253

QY 291 RGHRTQTVRL 300
Db 254 QNHQTQVRL 263

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## RESULT 12

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GHSR_RAT
ID GHSR_RAT STANDARD; PRT; 364 AA.
AC O08725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghsr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=97246555; PubMed=9092793; DOI=10.1210/me.11.4.415;
RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P.,
RA Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;
RT "Molecular analysis of rat pituitary and hypothalamic growth hormone
RT secretagogue receptors.";
RL Mol. Endocrinol. 11:415-423 (1997).
RN [2]
RP SEQUENCE OF 1-240 FROM N.A.
RC STRAIN=Wistar; TISSUE=Pituitary;
RX MEDLINE=98100386; PubMed=9437732; DOI=10.1016/S0196-9781(97)00263-5;
RA Yokote R., Sato M., Matsubara S., Ohye H., Niimi M., Murao K.,
RA Takahara J.;
RT "Molecular cloning and gene expression of growth hormone-releasing

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peptide receptor in rat tissues.";
Peptides 19:15-20 (1998).
[3]
RP FUNCTION.
RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230; Kangawa K.;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660 (1999).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U94321; AAC53156.1; -.
DR EMBL; AB001982; BAA31777.1; ALT_INIT.
DR RGD; 621397; Ghsr.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
KW DOMAIN 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT DOMAIN 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).
FT DOMAIN 97 117 Extracellular (Potential).
FT TRANSMEM 118 139 3 (Potential).
FT DOMAIN 140 162 Cytoplasmic (Potential).
FT TRANSMEM 163 183 4 (Potential).
FT DOMAIN 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT DOMAIN 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT DOMAIN 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT DOMAIN 327 364 Cytoplasmic (Potential).
FT DISULFID 115 197 By similarity.
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 364 AA; 40963 MW; DCBF559B5061EE9 CRC64;

Query Match 31.4%; Score 641; DB 1; Length 364;
Best Local Similarity 45.8%; Pred. No. 8.5e-36;
Matches 142; Conservative 41; Mismatches 65; Indels 62; Gaps 10;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGSG 55
Db 2 WNAT--PSEEPENVTLDLDWDASFGNDSLPDELPLFPAPLAGVTATCVATFVVGISG 59

QY 56 NVVTMLIGRYDMRTTNLYLGSMVAVSDLLILGLPFDLYLWRSRPPWFGPLLCRLSL 115
Db 60 NLLTMLVSRFRRLRTTNLYLSSMAFSDLLIFLCPLDLVLMQYRPNWFGDLLCKLFQ 119

QY 116 YVGECTYATLHMTALSVERYLACRPLRVLVTRRRVRLALAVLWALLSAGPFLF 175
Db 120 FVSECTYATVLTITALSVERYFAICFLPRAKVVTKGRKVLVILVAVAFCSAGPIFV 179

QY 176 LVGVQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSREC 235
Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQIGALVRLMVTYVTFPLCLSLYLGIGELWSSRRPLRGPAAAG---RE 290
Db 198 RATEFAVRSGLLTVNVMVSSVFFFLVFLVCLTVLYSLIGKLV--RR--RGDAAGVSSLD 253

QY 291 RGHRTQTVRL 300
Db 254 QNHQTQVRL 263

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FT	DOMAIN	67	72	Cytoplasmic (Potential).
FT	TRANSMEM	73	96	2 (Potential).
FT	DOMAIN	97	117	Extracellular (Potential).
FT	TRANSMEM	118	139	3 (Potential).
FT	DOMAIN	140	162	Cytoplasmic (Potential).
FT	TRANSMEM	163	183	4 (Potential).
FT	DOMAIN	184	211	Extracellular (Potential).
FT	TRANSMEM	212	235	5 (Potential).
FT	DOMAIN	236	263	Cytoplasmic (Potential).
FT	TRANSMEM	264	285	6 (Potential).
FT	DOMAIN	286	302	Extracellular (Potential).
FT	TRANSMEM	303	326	7 (Potential).
FT	DOMAIN	327	366	Cytoplasmic (Potential).
FT	DISULFID	116	198	By similarity.
FT	CARBOHYD	13	13	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	27	27	N-linked (GlcNAc. .) (Potential).
FT	VARSPLIC	266	289	AVVVFATFLICMLPHVGRYFSPKS -> GGSQCALELSLPG PLHSSCLFSSP (in isoform 1B). /FTid=VSP_001918.
FT	VARSPLIC	290	366	Missing (in isoform 1B). /FTid=VSP_001919.
FT	SEQUENCE	366 AA;	41194 MW;	2C850B3EF61B7C1C CRC64;
Query Match				
Best Local Similarity		31.4%;	Score 641;	DB 1; Length 366;
Matches 140;		Conservative 41;	Mismatches 70;	Indels 58; Gaps 8;
QY	5	WNGSDGPEGA-----REPPWPALPCD----	ERRCSPPLGALVPVTVAVCLCFWVGVSNG 56	
DB	2	WNATSEBPGPNLTLPDLCWDAPPENDSVLELLPLFP	TLLAGVTATCVALFVVGIAGN 61	
QY	57	VYVVMILGRYDRMTTNLYLGSMVSDLLILGLPDLVRLWRSRPWVFGPLLCRLSLY 116		
DB	62	LLTLMVWKRFRMRTTNLYLSSMAFSDLLIFLCMPDLDFRLWQYRPNLGNLLCKLQF 121		
QY	117	VCEGCTYATLLHMTALSVERVLAICRPLARVLVTRRVPZALAVLWAVALLSAGPFEL 176		
DB	122	VSESCYATVLTITALSVERYFAICFFPLRAKVVVTKGRVKLVILVIWAVAFCSAGPIFVL 181		
QY	177	VGVEQDPGISVVPGLNGTARIASSPPLMLSRAPPSPGSPETAEEAALFSSREC 236		
DB	182	VGVEHD-----NGT-----	DPED-----TNECR 199	
QY	237	PS--PAQLGALRVMLWVTAYFPFLFCLSLYGLIGRELWSSRRPLRGPAAG--RER 291		
DB	200	ATEPAVRSGLLTVMWSSVFFLPVCLTVLSLIGCKLW---RRKGEAAVGSLLRDQ 256		
QY	292	GHRQTVRVL 300		
DB	257	NHKQTVKML 265		
RESULT 14				
Q8MHZ5	PRELIMINARY;	PRT;	366 AA.	
AC	Q8MHZ5;			
DT	01-OCT-2002 (TReMBLrel. 22, Created)			
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)			
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DE	Grelin/growth hormone secretagogue receptor.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pituitary gland;			
RL	Murata T., Ikegami R., Morita Y., Shinozaki K.;			
RA	Submitted, (APR-2002) to the EMBL/GenBank/DBJ databases.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
DR	EMBL; AY093946; AAM19733.1; -.			

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DR EMBL; AY093949; AAM19734.1; --
DR EMBL; AY093950; AAM19735.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 366 AA; 41486 MW; 2F276651BC6C5D57 CRC64;

Query Match 29.7%; Score 607; DB 2; Length 366;
Best Local Similarity 42.2%; Pred. No. 1.8e-33;
Matches 129; Conservative 46; Mismatches 79; Indels 52; Gaps 6;

QY 5 WNGSDPE-----GAREPPWALPPCD---ERRCSFPPLGALVPYTVAVCLCLFVVGVSGN 56
Db 2 WNAITSEELGNLTLPDLWDADPNDLSLTDELPLFPAPLLAGVATTCVALFVVGIAGN 61
QY 57 VYVVMILGRYDRMTTNNLYLGLSMAVSDLLILLGLPFDLYRLWRGRPWVFGPPLCRLSLY 116
Db 62 LITLVLVSRFRRLTNNLYLGLSMAFSDLLIFLCPLDLVRLWYRPNWGLDCLKLQF 121
QY 117 VGEQCTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLMAVALLSAGPFLFL 176
Db 122 VSSECTYASVLTITALSVERYFAICFPLRAKVITKGRVKLVLAIVAVAFCSAWPIFML 181
QY 177 VGVQEDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPSGPETAEAAALFSRECR 236
Db 182 VGVHEH-----NGT-----DPRD-----TNECR 199
QY 237 PS--PAQLGALVLMVWTAYTFPLFLCLISILYGLIGRELMSRRPLRGPAASGRGRHR 294
Db 200 ATEFAVRSGLLTIWVWSSIFFFLVFCLTVLYSLIGKLMRRRSEVVVGASLSDQNHK 259
QY 295 QTVRVL 300
Db 260 QTVKML 265

RESULT 15
Q711Q7 PRELIMINARY; PRT; 215 AA.
AC Q711Q7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative growth hormone secretagogue receptor 1a (Fragment).
GN Name=GHS1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=22874034; PubMed=14511987; DOI=10.1016/S0016-6480(03)00250-8;
RA Geelissen S.M.E., Beck I.M.E., Darras V.M., Kuhn E.R.,
RA Van der Geyten S.;
RT "Distribution and regulation of chicken growth hormone secretagogue
receptor isoforms."
RL Gen. Comp. Endocrinol. 134:167-174 (2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AJ309543; CAC29062.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 215 AA; 24487 MW; 68BCE14DFE81DEF5 CRC64;

Query Match 21.7%; Score 444; DB 2; Length 215;
Best Local Similarity 40.7%; Pred. No. 1.3e-22;
Matches 85; Conservative 45; Mismatches 35; Indels 44; Gaps 4;

QY 97 RLWRSRPWFGPPLCRLSLYVGEQCTYATLLHMTALSVERYLAICRPLARVLVTRRRVR 156
Db 1 RLWQYRPWNFGDLLCKLQFQISECTYSTILNITALSVERYVAICFPLRAKVIITKRVK 60
QY 157 ALIAVLMAVALLSAGPFLFLVGVQEDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPP 216
Db 61 LVILILWAVSPISAGPIFVLGVHE-----NGT-----NPLSTN----- 95
QY 217 SPSPGPETAEEAALFSRECRPSAQL--GALRVMLVWTAYTFPLFLCLISILYGLIGREL 274
Db 96 -----ECRATEYAIRSGLLTIMVWISSIFFFLVFCLTVLYSLIGRKL 138
QY 275 WSSRRRLRGPAASGRGRHROTVRVLRKW 303
Db 139 WRRKKNIGPSTIIRDKNNKQTVKMLGRY 167
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Search completed: April 11, 2005, 21:04:56  
Job time : 63.3985 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:55 ; Search time 503.911 Seconds  
(without alignments)  
9955.765 Million cell updates/sec

Title: US-09-719-485-1  
Perfect score: 3066  
Sequence: 1 ttgaattatctgtcactg.....acgtgaacgatgggataa 3066

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCUTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	9.2	283	US-08-993-088A-4	Sequence 4, Appli
2	283	9.2	283	US-08-993-424B-4	Sequence 4, Appli
3	283	9.2	283	US-09-603-680-4	Sequence 4, Appli
4	248.2	8.1	1050	US-09-762-661A-1	Sequence 1, Appli
5	234.8	7.7	1063	US-09-077-675A-1	Sequence 1, Appli
6	234.8	7.7	1063	US-09-077-674-1	Sequence 1, Appli
7	231.6	7.6	1095	US-09-743-475-2	Sequence 2, Appli
8	231.6	7.6	4009	US-09-743-475-1	Sequence 1, Appli
9	230	7.5	1029	US-09-077-675A-4	Sequence 4, Appli
10	230	7.5	1029	US-09-077-674-4	Sequence 4, Appli
11	229	7.5	250	US-09-016-434-359	Sequence 359, App
12	228.8	7.5	1122	US-09-077-675A-9	Sequence 9, Appli
13	228.8	7.5	1122	US-09-077-674-9	Sequence 15, Appl
14	228.4	7.4	1092	US-09-077-674-15	Sequence 15, Appl
15	228.4	7.4	1092	US-09-077-675A-14	Sequence 14, Appl
16	228.4	7.4	3129	US-09-077-674-14	Sequence 14, Appl
17	228.4	7.4	3129	US-09-077-675A-6	Sequence 6, Appli
18	227.8	7.4	1088	US-09-077-674-6	Sequence 6, Appli
19	227.8	7.4	1088	US-09-016-434-1148	Sequence 1148, Ap
20	227.8	7.4	1101	US-09-170-496D-87	Sequence 87, Appl
21	227.8	7.4	1101	US-09-364-425B-44	Sequence 44, Appl
22	227.8	7.4	1101	US-09-949-016-15317	Sequence 15317, A
23	227.8	7.4	37004	US-09-729-995-3	Sequence 3, Appli
24	206.8	6.7	37004	US-10-135-689-3	Sequence 3, Appli
25	202.2	6.6	29629	US-10-690-617-3	Sequence 3, Appli
26	202.2	6.6	29629		
27	202.2	6.6	29629		

ALIGNMENTS

RESULT 1

US-08-993-088A-4  
Sequence 4, Application US/08993088A  
Patent No. 6287855

GENERAL INFORMATION:

APPLICANT: Tan Carina  
APPLICANT: Sullivan, Kathleen  
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND  
NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,088A

FILING DATE: 18-DEC-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/033,851

FILING DATE: 27-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 19846

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-1958

TELEFAX: 732-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 283 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Other

LOCATION: 1...283

OTHER INFORMATION: cdna probe

US-08-993-088A-4

Sequence 16038, A  
Sequence 165371,  
Sequence 16402, A  
Sequence 15870, A  
Sequence 165372,  
Sequence 165373,  
Sequence 13555, A  
Sequence 77323, A  
Sequence 14000, A  
Sequence 12517, A  
Sequence 16021, A  
Sequence 14577, A  
Sequence 14578, A  
Sequence 77324, A  
Sequence 12683, A  
Sequence 13194, A  
Sequence 77322, A  
Sequence 13220, A

Query Match 9.2%; Score 283; DB 3; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.3e-49;  
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1234 TGGGACACCAACAACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTCTGC 1293  
DB 1 TGGGACACCAACCACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTCTGC 60

QY 1294 TGGGCTGCGGTTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 1353  
DB 61 TGGGCTGCGGTTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 120

QY 1354 TGCTCTGCGGCTGTCCCTCTACGTGGGCGAGGCTGCACCTACGCCACGCTGTGTGCACA 1413  
DB 121 TGCTCTGCGGCTGTCCCTCTACGTGGGCGAGGCTGCACCTACGCCACGCTGTGTGCACA 180

QY 1414 TGACCGCGCTCAGCGTTCGAGCGTACCTGGGCACTTCGCCCGCTTCGCGCCCGCGTCT 1473  
DB 181 TGACCGCGCTCAGCGTTCGAGCGTACCTGGGCACTTCGCCCGCTTCGCGCCCGCGTCT 240

QY 1474 TGGTACCGCGCGCGCTTCGCGCGCTCATCGTGTGTCTGTG 1516  
DB 241 TGGTACCGCGCGCGCTTCGCGCGCTCATCGTGTGTCTGTG 283

## RESULT 2

US-08-993-424B-4  
; Sequence 4, Application US/08993424B  
; Patent No. 6337206  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Kolakowski, Lee F., Jr.  
; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/993,424B  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846NP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1...283  
; OTHER INFORMATION: cdna probe

## US-08-993-424B-4

Query Match 9.2%; Score 283; DB 3; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.3e-49;  
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1234 TGGGACACCAACAACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTCTGC 1293  
DB 1 TGGGACACCAACCACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTCTGC 60

QY 1294 TGGGCTGCGGTTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 1353  
DB 61 TGGGCTGCGGTTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 120

QY 1354 TGCTCTGCGGCTGTCCCTCTACGTGGGCGAGGCTGCACCTACGCCACGCTGTGTGCACA 1413  
DB 121 TGCTCTGCGGCTGTCCCTCTACGTGGGCGAGGCTGCACCTACGCCACGCTGTGTGCACA 180

QY 1414 TGACCGCGCTCAGCGTTCGAGCGTACCTGGGCACTTCGCCCGCTTCGCGCCCGCGTCT 1473  
DB 181 TGACCGCGCTCAGCGTTCGAGCGTACCTGGGCACTTCGCCCGCTTCGCGCCCGCGTCT 240

QY 1474 TGGTACCGCGCGCGCTTCGCGCGCTCATCGTGTGTCTGTG 1516  
DB 241 TGGTACCGCGCGCGCTTCGCGCGCTCATCGTGTGTCTGTG 283

## RESULT 3

US-09-603-680-4  
; Sequence 4, Application US/09603680  
; Patent No. 6544753  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Sullivan, Kathleen  
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/603,680  
; FILING DATE: 26-Jun-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; APPLICATION NUMBER: 08/993,088  
; FILING DATE: 18-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846 CA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other

[illegible]





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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4009
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-743-475-1

Query Match          7.6%; Score 231.6; DB 4; Length 4009;
Best Local Similarity 68.8%; Pred. No. 1.7e-38;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY      1120  CGCCCTTTCCCTGGGGCGCTGGTGCCCGGTGACCGCTGTGTCCTGTGCTCTTTCTGTCG 1179
DB      605  CACTGTTCCCGCGCGCTGCTGGCGGGCGTCACTGCCACCTGCGTGGCGCTCTTCGTGG 664

QY      1180  TCGGGGTGAGCGGCAACGTGGTGACCGTGATCTGATCGGGCGCTACCGGACATCGGGA 1239
DB      665  TGGGCGATCTTGGGGCAACCTGCTCAACATGCTGGTGTGCCCGCTTCCGGAGCTCGGCA 724

QY      1240  CCACACCAACCTTGTAACCTGGGCAGCATGGCGGTGCCGACCTACTCATCTGCTCGGGC 1299
DB      725  CCACACCAACCTCTACCTATATCCAGCATGGCGCTTCTCCGATCTGCTCATCTTCTGTGCA 784

QY      1300  TGCCGTTGACCTGTACCGCTCTGGCGCTCGCGGCTTGGGTGTTCGGGCGCTGCTCT 1359
DB      785  TGCCGCTGACCTCTGTCGGCTCTGGCAGTATCGGCGCTTGGAACTTCGGCGACCTGCTCT 844

QY      1360  GCGCGCTGTCCTCTTACGTGGCGAGGGGTGCACTTACGCCACGCTGCTGCACATGACCG 1419
DB      845  GCAAACTCTTCAGTTTGTACGGAGAGGTGCACTTACGCCACGCTCTTCAACNTACCG 904

QY      1420  CGCTCAGCGTCAAGCGCTACTTGGCCATCTGCGGCCGCTTCGCGGCCCGCGTCTTGGTCA 1479
DB      905  CGCTCAGCGTCAAGCGCTACTTTCGCCATCTGCTTCCCGCTGGGGGCCAAGGTGGTGTCA 964

QY      1480  CCGCGCGCGCGCTCCGCGGCTCATCGCTGCTCTTGGGCGGTGGGCGTCTCTCTGCCG 1539
DB      965  CCAAGGCGCGTGAAGCTGTGATCTTGTATCTGGGCGCGTGGCTTCTGAGCGCGG 1024

QY      1540  GTCCCTCTTGTCTCTGTGGCGCTGAGCAGAACCCCGCA 1581

DB      1025  GSCCATCTTTCGTGTGGTGGCGCTGGAGCAGAGAACCGCA 1066

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RESULT 9
US-09-077-675A-4
; Sequence 4, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TFPINOT01
; CLONE: 2018536
; US-09-016-434-359

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Qy	2884	ATCCTCTACAACCTCATTTCAAGAGAGTACAGAGCGCGCCCTTTAAACTGCTGCTCGCA	2943	
Db	61	ATCCTCTACAACCTCATTTCAAGAGAGTACAGAGCGCGCCCTTTAAACTGCTGCTCGCA	120	
Qy	2944	AGGAAGTCCAGGCGGAGAGGCTTCCACAGAAGCAGAGGACACTCGCGGGGAAGTTGCAGGG	3003	
Db	121	AGNAGTCCAGGCGGAGAGG-TTCCACAGAAGCAGAGGACACTCGCGGGGAAGTTGCAGGG	179	
Qy	3004	GACACTGGAGGAGACACGCTGGGCTACACCGAGACAAGCGCTTAACGTGAAGACGATGGGA	3063	
Db	180	GACACTGGAGGAGACACGCTGGGCTACACCGAGACAGCGCTTAACGTGAAGACGATGGGA	239	
Qy	3064	TAA 3066		
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RESULT 12  
US-09-077-675A-9  
; Sequence 9, Application US/09077675A

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; Patent No. 6242199
;
; GENERAL INFORMATION:
;
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Feighner, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
;
; TITLE OF INVENTION: RECEPTOR ASSAY
;
; NUMBER OF SEQUENCES: 16
;
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
;
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
;
; TELEX:
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; INFORMATION FOR SEQ ID NO: 9:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1122 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
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; US-09-077-675A-9

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[illegible]





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Db      404  CGCTGAGCGTCGAGCGCTACTTCGCCATCTGCTTCCCTCTGCGGCCCAAGGTGGTGTCA 463
Qy      1480  CCGCGCGCGCTCGCGCGCTCATCGCTGTGCTCTGGGCCGCTGGCGCTCTCTGCGG 1539
Db      464  CTAAGGGCCGCTGAAGCTGGTCATCTTGTATCTGGGCCGTGGCTTCTGCAGCGCGG 523
Qy      1540  GTCCCTTCTTGTCTGTGGCGCTCGAGCAGACCCCGGCA 1581
Db      524  GGCCCATCTTCGTGTGTGGCGCTGGAGCAGCAAAACGGCA 565
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Job time : 506.911 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 06:41:42 ; Search time 1790.07 Seconds  
(without alignments)  
10379.464 Million cell updates/sec

Title: US-09-719-485-1

Perfect score: 3066

Sequence: 1 ttgaattatctgtcactg.....acgtgaagacatgggataa 3066

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2021.2	65.9	2040	18	US-10-723-955-129
4	2013.2	65.7	2040	17	US-10-417-820A-151
5	1038	33.9	1161	18	US-10-679-813-11
6	901	29.4	1239	15	US-10-225-567A-472
7	901	29.4	1239	15	US-10-290-078-13
8	901	29.4	1239	15	US-10-290-078-14
9	901	28.4	1239	16	US-10-206-677-1
10	901	29.4	1239	18	US-10-679-813-9
c 11	761.4	24.8	1179	18	US-10-363-345A-33737

c 12	761.4	24.8	1179	18	US-10-363-345A-33738	Sequence 33738, A
c 13	761.4	24.8	1179	19	US-10-363-483A-33737	Sequence 33737, A
c 14	761.4	24.8	1179	19	US-10-363-483A-33738	Sequence 33738, A
c 15	722	23.5	1179	18	US-10-363-345A-33739	Sequence 33739, A
c 16	722	23.5	1179	18	US-10-363-345A-33740	Sequence 33740, A
c 17	722	23.5	1179	19	US-10-363-483A-33739	Sequence 33739, A
c 18	722	23.5	1179	19	US-10-363-483A-33740	Sequence 33740, A
c 19	234.8	7.7	1063	16	US-10-303-204A-1	Sequence 1, Appli
c 20	230	7.5	1029	16	US-10-303-204A-4	Sequence 4, Appli
c 21	229	7.5	250	17	US-10-305-720-359	Sequence 359, App
c 22	228.8	7.5	870	15	US-10-225-567A-139	Sequence 139, App
c 23	228.8	7.5	1122	16	US-10-303-204A-9	Sequence 9, Appli
c 24	228.4	7.4	1092	16	US-10-303-204A-15	Sequence 15, Appl
c 25	228.4	7.4	3129	16	US-10-303-204A-14	Sequence 14, Appl
c 26	227.8	7.4	1088	16	US-10-303-204A-6	Sequence 6, Appli
c 27	227.8	7.4	1101	15	US-10-251-385-87	Sequence 87, Appl
c 28	227.8	7.4	1101	15	US-10-251-385-209	Sequence 209, App
c 29	227.8	7.4	1101	16	US-10-276-392-22	Sequence 22, Appl
c 30	227.8	7.4	1101	17	US-10-305-720-1148	Sequence 1148, Ap
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c 33	205.2	6.7	5157	17	US-10-242-515-2605	Sequence 2605, Ap
c 34	205.2	6.7	5199	9	US-09-764-877-2607	Sequence 2607, Ap
c 35	205.2	6.7	5199	17	US-10-242-515-2607	Sequence 2607, Ap
c 36	202.2	6.6	29629	9	US-09-729-995-3	Sequence 3, Appli
c 37	202.2	6.6	29629	13	US-10-135-689-3	Sequence 3, Appli
c 38	202.2	6.6	29629	17	US-10-690-617-3	Sequence 3, Appli
c 39	201.8	6.6	12822	9	US-09-764-847-1579	Sequence 1579, Ap
c 40	201.8	6.6	12822	14	US-10-092-154-1579	Sequence 1579, Ap
c 41	201.2	6.6	953	13	US-10-027-632-248867	Sequence 248867, A
c 42	201.2	6.6	953	17	US-10-027-632-248867	Sequence 248867, A
c 43	201	6.6	26667	18	US-10-741-601-5709	Sequence 5709, Ap
c 44	201	6.6	26667	19	US-10-741-600-17811	Sequence 17811, A
c 45	200.8	6.5	704	13	US-10-027-632-125989	Sequence 125989, A

#### ALIGNMENTS

#### RESULT 1

US-09-876-252-129  
; Sequence 129, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Receptor  
; FILE REFERENCE: AREN-0054  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948

	Query Match	65.9%	Score	2021.2;	DB	10;	Length	2040;	
	Best Local Similarity	99.8%	Pred.	No. 0;					
	Matches	2035;	Conservative	0;	Mismatches	3;	Indels	2;	Gaps
		1;							
Qy	1029	ATGGGAGCCCCCTGGGAACGACGACGGCGCCCGAGGGGGCGCGGAGCGCCGCTGGCCCC	1088						
Db	1	ATGGGAGCCCCCTGGGAACGACGACGGCGCCCGAGGGGGCGCGGAGCGCCGCTGGCCCC	60						
Qy	1089	GCCTGTGCGCGCTTTCGACGACGACGCGCTGCTCGCGCTTTCCTTGGGGGGCGCTGGTGC	1148						
Db	61	GCCTGTGCGCGCTTTCGACGACGACGCGCTGCTCGCGCTTTCCTTGGGGGGCGCTGGTGC	120						
Qy	1149	GTGACCGCTGTGTGCTGTGCTGTTCGTTCGTTCGGGGTGAACGGCAACCTGGTGTGACCGTG	1208						
Db	121	GTGACCGCTGTGTGCTGTGCTGTTCGTTCGTTCGGGGTGAACGGCAACCTGGTGTGACCGTG	180						
Qy	1209	ATGCTGATCGGGCGCTACCGGGACATCGGACACACCAACCTTGTTACCTGGGCAACGATG	1268						
Db	181	ATGCTGATCGGGCGCTACCGGGACATCGGACACCAACCACTTGTACCTTGGGCAACGATG	240						
Qy	1269	GCCGTGTCCGACCTTACTCATCTCTGCTCGGGCTGCGCTTCGACCTGTATACCGCTCTTGGCGC	1328						





QY 1809 CTGTCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGGAGCAGCGCGGGCGG 1868  
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGGAGCAGCGCGGGCGG 840  
QY 1869 CTGCGAGCGCGGGCGCTCGGGGGGAGAGAGGCGCACCGGCGAGCGCTCGGGTCTGT 1928  
Db 841 CTGCGAGCGCGGGCGCTCGGGGGGAGAGAGGCGCACCGGCGAGCGCTCGGGTCTGT 900  
QY 1929 CGTAAGTGGAGCGCGGTGGTTCACAGACGCTGTGAGTCCGCGCGCGGGGAGC 1988  
Db 901 CGTAAGTGGAGCGCGGTGGTTCACAGACGCTGTGAGTCCGCGCGCGGGGAGC 960  
QY 1989 GGGCAACGCTGGGTCCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 2048  
Db 961 GGGCAACGCTGGGTCCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 1020  
QY 2049 --TCCTATTTCCGATTCAGGCTCCACCGCGCGGTACTTCCCATCCCCCGAGAAACCATG 2106  
Db 1021 TTTCTATTTCCGATTCAGGCTCCACCGCGCGGTACTTCCCATCCCCCGAGAAACCATG 1080  
QY 2107 TCCTGTCCCCAGGAGCTCTGGGAGACCCAGGCGCTTTGAGGTGGGATCCCGGATC 2166  
Db 1081 TCCTGTCCCCAGGAGCTCTGGGAGACCCAGGCGCTTTGAGGTGGGATCCCGGATC 1140  
QY 2167 CGATTCAAGTAACAGAGTGTCTTCCAGAGCTCTGAGACAGAAAGAGAGTTGGTAA 2226  
Db 1141 CGATTCAAGTAACAGAGTGTCTTCCAGAGCTCTGAGACAGAAAGAGAGTTGGTAA 1200  
QY 2227 TTTCTTAATCCAAACCACTGTTAGATGCCACAAATGAGGAGTCTCCACAGTGTCTTGAGA 2286  
Db 1201 TTTCTTAATCCAAACCACTGTTAGATGCCACAAATGAGGAGTCTCCACAGTGTCTTGAGA 1260  
QY 2287 AGACGAGGAGATTTCAATTAAGCTAAATTTTTTAATTTTAATTTAAGTGAATGCTGAAGC 2346  
Db 1261 AGACGAGGAGATTTCAATTAAGCTAAATTTTTTAATTTAATTTAAGTGAATGCTGAAGC 1320  
QY 2347 TAAAGTAAACCTGTCTGATCAAAAGTAAAGATTGTGCACAGCTGTGTAGATTTCT 2406  
Db 1321 TAAAGTAAACCTGTCTGATCAAAAGTAAAGATTGTGCACAGCTGTGTAGATTTCT 1380  
QY 2407 TTCAACAGAGAACAGAAAACTTGTCTCCGAAGTGGTGTGTGGAAGGAGCCTGCCAAG 2466  
Db 1381 TTCAACAGAGAACAGAAAACTTGTCTCCGAAGTGGTGTGTGGAAGGAGCCTGCCAAG 1440  
QY 2467 CGGCTTGTTCAGAGAAATGCTCTCTGTTATGTCAGCTTGATACACATATGG 2526  
Db 1441 CGGCTTGTTCAGAGAAATGCTCTCTGTTATGTCAGCTTGATACACATATGG 1500  
QY 2527 AGCTACTATGCAAGTTTAAAGCAAGTATCCATGACAGCTGAGCCTGTCTATTTTCT 2586  
Db 1501 AGCTACTATGCAAGTTTAAAGCAAGTATCCATGACAGCTGAGCCTGTCTATTTTCT 1560  
QY 2587 GGGGTGAGGATCTGCTAGTAGAAGTTTCTCTAATTTATTTTGTGTGTGTATTTCT 2646  
Db 1561 GGGGTGAGGATCTGCTAGTAGAAGTTTCTCTAATTTATTTTGTGTGTATTTCT 1620  
QY 2647 GCAGATGTTCTTGTCTGGGGTGGGGGTTATTTCTTCCCAATGCTTTTGTATATCCC 2706  
Db 1621 GCAGATGTTCTTGTCTGGGGTGGGGGTTATTTCTTCCCAATGCTTTTGTATATCCC 1680  
QY 2707 GGTGCTGTCTTATGTTGAGTGGTGGTGGTCTGCGCATTTATATTTGCTGGTTCGCC 2766  
Db 1681 GGTGCTGTCTTATGTTGAGTGGTGGTGGTCTGCGCATTTATATTTGCTGGTTCGCC 1740  
QY 2767 TTCCAGTGTGGCAGATCATTTATATAACACAGGAAGATTCCGGATGATGATCTCTCT 2826  
Db 1741 TTCCAGTGTGGCAGATCATTTATATAACACAGGAAGATTCCGGATGATGATCTCTCT 1800  
QY 2827 CAGTACTTTTAAATCGTCTGCAACTTTTCTATCTGAGCGCATCTATCAACCCCAATC 2886  
Db 1801 CAGTACTTTTAAATCGTCTGCAACTTTTCTATCTGAGCGCATCTATCAACCCCAATC 1860  
QY 2887 CTCTACAACCTCATTTTCAAGAAAGTACAGAGCGCGGCGCTTTTAACTGTGCTCGCAAG 2946

Db 1861 CTCTACAACCTCATTTTCAAGAAAGTACAGAGCGCGGCGCTTTTAACTGTGCTCGCAAG 1920  
QY 2947 AAGTCAGGCGCGAGAGGCTTCCACAGAGCAGGAGCACTGCGGGGGAAGTTGCAGGGGAC 3006  
Db 1921 AAGTCAGGCGCGAGAGGCTTCCACAGAGCAGGAGCACTGCGGGGGAAGTTGCAGGGGAC 1980  
QY 3007 ACTGGAGGAGACAGGTTGGGCTACACGAGACAAGGCTTAACGTGAAGACGATGGGATAA 3066  
Db 1981 ACTGGAGGAGACAGGTTGGGCTACACGAGACAAGGCTTAACGTGAAGACGATGGGATAA 2040

RESULT 3  
US-10-723-955-129  
; Sequence 129, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinsma, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US29.CON  
; CURRENT APPLICATION NUMBER: US/10/723,955  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 10/417,820  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 129  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-955-129

Query Match 65.9%; Score 2021.2; DB 18; Length 2040;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2035; Conservative 0; Mismatches 3; Indels 2; Gaps 1;  
QY 1029 ATGCGACGCCCTCGAAGCAGGACGCGCCCGAGGGGCGCGGAGCGCGCGTGGGCC 1088  
Db 1 ATGCGGAGCGCCCTCGAAGCAGGACGCGCCCGAGGGGCGCGGAGCGCGCGTGGGCC 60  
QY 1089 GCGCTGCGCGCTTGGAGCGAGCGCGCTGCTCGCCCTTTCCCTGGGGCGCTGTGCGG 1148  
Db 61 GCGCTGCGCGCTTGGAGCGAGCGCGCTGCTCGCCCTTTCCCTGGGGCGCTGTGCGG 120

Qy	1149	GTGACCGCTGTGTGCTGTGCTGTTTCTGTCGTGCGGGTGAGCGCAACAGTGTGACCGGTG	1201
Db	121	GTGACCGCTGTGTGCTGTGCTGTTTCTGTCGTGCGGGTGAGCGCGCAACAGTGTGACCGGTG	180
Qy	1209	ATGCTGATCGGGCGCTACCGGGACATCGGACACACCAACCTGTACCTTGGCAGCATG	1268
Db	181	ATGCTGATCGGGCGCTACCGGGACATCGGACACACCAACCTGTACCTTGGCAGCATG	240
Qy	1269	GCCGTGTCGACCTTACTCATCTCTCGGGCTGCGCTTTCGACCTGTACCGCCTCTGGCGC	1328
Db	241	GCCGTGTCGACCTTACTCATCTCTCGGGCTGCGCTTTCGACCTGTACCGCCTCTGGCGC	300
Qy	1329	TGCGGGCCCTGGGGTGTGGGGCCGCTGCTGTGCGCCCTGTCCCTCTACGTGAGGCGAGGGC	1388
Db	301	TGCGGGCCCTGGGGTGTGGGGCCGCTGCTGTGCGCCCTGTCCCTCTACGTGAGGCGAGGGC	360
Qy	1389	TGCACCTACGCCACGCTCTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTTGGCCATC	1448
Db	361	TGCACCTACGCCACGCTCTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTTGGCCATC	420
Qy	1449	TGCCGCCCGCTCCGCGCCCGCTCTTGCTCAACCGCGCGCGCTCCGCGGCTCATCGCT	1508
Db	421	TGCCGCCCGCTCCGCGCCCGCTCTTGCTCAACCGCGCGCGCTCCGCGGCTCATCGCT	480
Qy	1509	GTGCTCTGGGCGTGGGCGCTGCTCTGTGCGGTCCTCTTGTGTCGTGGGCGTGCAG	1568
Db	481	GTGCTCTGGGCGTGGGCGCTGCTCTGTGCGGTCCTCTTGTGTCGTGGGCGTGCAG	540
Qy	1569	CAGAACCCCGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGGATCGGCTCTCTG	1628
Db	541	CAGAACCCCGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGGATCGGCTCTCTG	600
Qy	1629	CCTCTCGCTCTGTCGCGCCTCTCTGCTCTCGGGCGGCACCGCGCTCCCGCGCTCG	1688
Db	601	CCTCTCGCTCTGTCGCGCCTCTCTGCTCTCGGGCGGCACCGCGCTCCCGCGCTCG	660
Qy	1689	GGGCCCCGAGACCGCGGAGCGCGGCGCTGTTCAGCCGCGAATGCGCGCCGAGCCCGCG	1748
Db	661	GGGCCCCGAGACCGCGGAGCGCGGCGCTGTTCAGCCGCGAATGCGCGCCGAGCCCGCG	720
Qy	1749	CAGCTGGGGCGGCTGCGGTGCATGCTGTGGTCAACCGGCTACTTCTTCTGCGCCTTT	1808
Db	721	CAGCTGGGGCGGCTGCGGTGCATGCTGTGGTCAACCGGCTACTTCTTCTGCGCCTTT	780
Qy	1809	CTGTGCTCTCAGCATCTCTACGGCTCATCGGGCGGAGCTGTGAGCAGCAGCGCGCGCG	1868
Db	781	CTGTGCTCTCAGCATCTCTCTACGGCTCATCGGGCGGAGCTGTGAGCAGCAGCGCGCGCG	840
Qy	1869	CTCGAGGCCCGGCGCTCTCGGGCGGGAGAGGCCACCGGAGAGCGCTCCGCTGCTG	1928
Db	841	CTCGAGGCCCGGCGCTCTCGGGCGGGAGAGAGGCCACCGGAGAGCGCTCCGCTGCTG	900
Qy	1929	CGTAAGTGGAGCCGCGCTGGTTCCAAAGAGCCTGCTGAGTCGCGCCCGCGCGGGAGC	1988
Db	901	CGTAAGTGGAGCCGCGCTGGTTCCAAAGAGCCTGCTGAGTCGCGCCCGCGCGGGAGC	960
Qy	1989	GCGCAACGCTGGTCCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCCC	2048
Db	961	GCGCAACGCTGGTCCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCCC	1020
Qy	2049	--TCTATTTCGATTCCAGCTCCACCGCGCGGTACTTCCATCCCCCGAGAAAACCATG	2106
Db	1021	TTTCTATTTCGATTCCAGCTCCACCGCGCGGTACTTCCATCCCCCGAGAAAACCATG	1080
Qy	2107	TCTGTCCCCAGAGCTCTGGGGGACCCAGAGGCGCTTTTGTAGGTTGGGATCTCCCGGATC	2166
Db	1081	TCTGTCCCCAGAGCTCTGGGGGACCCAGAGGCGCTTTTGTAGGTTGGGATCTCCCGGATC	1140
Qy	2167	CGATTCTAGTAACAGCAGTCTTTTTCAGAGCCTCTCAGACCCAGAAAGGAGAGTTGGTAA	2226
Db	1141	CGATTCTAGTAACAGCAGTCTTTTTCAGAGCCTCTCAGACCCAGAAAGGAGAGTTGGTAA	1200
Qy	2227	TTCTTAAATCAACCAACCTGTTAGATGCCAAATAGGAGTCTCTCAGTGTCTTTTGAGA	2286

## RESULT 4

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US-10-417-820A-151
; Sequence 151, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaow, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; RECEPTORS
; FILE REFERENCE: 7. US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12

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ORGANISM: Homo sapiens  
US-10-225-567A-472

Query Match 29.4%; Score 901; DB 15; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 6.4e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1029 ATGGGACCCCTGGAACGGCAGCGAGCGCGCCCGGAGGGGGCGCGGAGCGCCCGTGGGCC 1088  
DB 1 ATGGGACCCCTGGAACGGCAGCGAGCGCGCCCGGAGGGGGCGCGGAGCGCCCGTGGGCC 60

QY 1089 GCGTGGCCCTTGGCAGCGCGCGTGTCTGCGCCCTTTCCCTTGGGGCGCTGTGGCG 1148  
DB 61 GCGTGGCCCTTGGCAGCGCGCGTGTCTGCGCCCTTTCCCTTGGGGCGCTGTGGCG 120

QY 1149 GTGACCGCTGTGGCTGTGCTGTCTGCGGGGTGAGGGGCAAGTGGTACCGTG 1208  
DB 121 GTGACCGCTGTGGCTGTGCTGTCTGCGGGGTGAGGGGCAAGTGGTACCGTG 180

QY 1209 ATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACCACTTGTACTGGGAGCATG 1268  
DB 181 ATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACCACTTGTACTGGGAGCATG 240

QY 1269 GCGGTGTCGACCTACTCATCTGCTCGGGGTGCGCTGTGACCTGTACCGCTCTGGCGC 1328  
DB 241 GCGGTGTCGACCTACTCATCTGCTCGGGGTGCGCTGTGACCTGTACCGCTCTGGCGC 300

QY 1329 TCGGGCCCTGGGTGTTGGGGCGCGTGTCTGCGCCCTTTCCCTTGGGGCGCTGTGGCG 1388  
DB 301 TCGGGCCCTGGGTGTTGGGGCGCGTGTCTGCGCCCTTTCCCTTGGGGCGCTGTGGCG 360

QY 1389 TGCACCTACGCGACCTGCTGCATACCGCGCTCAGCGCTACCTGAGCGCTACTGGCCATC 1448  
DB 361 TGCACCTACGCGACCTGCTGCATACCGCGCTCAGCGCTACCTGAGCGCTACTGGCCATC 420

QY 1449 TGGCCCGCTCGCGCGCGGTGTTGGTACCGCGCGCGGTCCCGCGCGCTCATCGCT 1508  
DB 421 TGGCCCGCTCGCGCGCGGTGTTGGTACCGCGCGCGGTCCCGCGCGCTCATCGCT 480

QY 1509 GTGCTCTGGCGCGTGGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 1568  
DB 481 GTGCTCTGGCGCGTGGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 540

QY 1569 CAGGACCCCGCATCTCCGTAGTCCGGGCGCTCAATGGCACCGCGCGATCGCTTCTCG 1628  
DB 541 CAGGACCCCGCATCTCCGTAGTCCGGGCGCTCAATGGCACCGCGCGATCGCTTCTCG 600

QY 1629 CCTCTGCGCTGTGCGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 1688  
DB 601 CCTCTGCGCTGTGCGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 660

QY 1689 GGGCCCGAGACCGCGAGCGCGCGGTGTTGAGCGGAAATGCGGCGGAGCCCGCG 1748  
DB 661 GGGCCCGAGACCGCGAGCGCGCGGTGTTGAGCGGAAATGCGGCGGAGCCCGCG 720

QY 1749 CAGCTGGGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1808  
DB 721 CAGCTGGGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780

QY 1809 CTGTGCTCAGCATCTCTACCGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCG 1868  
DB 781 CTGTGCTCAGCATCTCTACCGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCG 840

QY 1869 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGCGCAACCGCGAGCGTCCGCGTCTG 1928  
DB 841 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGCGCAACCGCGAGCGTCCGCGTCTG 900

1929 C 1929  
901 C 901

RESULT 7

US-10-290-078-13  
Sequence 13, Application US/10290078  
Publication No. US20030124596A1

GENERAL INFORMATION:  
APPLICANT: Carroll, Joseph A.  
TITLE OF INVENTION: Methods and Compositions for Treating  
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
FILE OF INVENTION: 14395, 14618, 17692 or 58874  
FILE REFERENCE: MPI2001-288P1(M)  
CURRENT APPLICATION NUMBER: US/10/290,078  
CURRENT FILING DATE: 2002-11-07

NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 1239  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-290-078-13

Query Match 29.4%; Score 901; DB 15; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 6.4e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1029 ATGGGACCCCTGGAACGGCAGCGAGCGCGCCCGGAGGGGGCGCGGAGCGCCCGTGGGCC 1088  
DB 1 ATGGGACCCCTGGAACGGCAGCGAGCGCGCCCGGAGGGGGCGCGGAGCGCCCGTGGGCC 60

QY 1089 GCGTGGCCCTTGGCAGCGCGCGTGTCTGCGCCCTTTCCCTTGGGGCGCTGTGGCG 1148  
DB 61 GCGTGGCCCTTGGCAGCGCGCGTGTCTGCGCCCTTTCCCTTGGGGCGCTGTGGCG 120

QY 1149 GTGACCGCTGTGCTGTGCTGTCTGCTGCGGGGTGAGCGGCAACGTGGTACCGTG 1208  
DB 121 GTGACCGCTGTGCTGTGCTGTCTGCTGCGGGGTGAGCGGCAACGTGGTACCGTG 180

QY 1209 ATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACCACTTGTACTGGGAGCATG 1268  
DB 181 ATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACCACTTGTACTGGGAGCATG 240

QY 1269 GCGGTGTCGACCTACTCATCTGCTCGGGGTGCGCTGTGACCTGTACCGCTCTGGCGC 1328  
DB 241 GCGGTGTCGACCTACTCATCTGCTCGGGGTGCGCTGTGACCTGTACCGCTCTGGCGC 300

QY 1329 TCGGGCCCTGGGTGTTGGGGCGCGTGTCTGCGCCCTTTCCCTTGGGGCGAGGCG 1388  
DB 301 TCGGGCCCTGGGTGTTGGGGCGCGTGTCTGCGCCCTTTCCCTTACGTGGGCGAGGCG 360

QY 1389 TGCACCTACGCGACCTGCTGCATACCGCGCTCAGCGCTACCTGAGCGCTACTGGCCATC 1448  
DB 361 TGCACCTACGCGACCTGCTGCATACCGCGCTCAGCGCTACCTGAGCGCTACTGGCCATC 420

QY 1449 TGGCCCGCTCGCGCGCGGTGTTGGTACCGCGCGCGGTCCCGCGCGCTCATCGCT 1508  
DB 421 TGGCCCGCTCGCGCGCGGTGTTGGTACCGCGCGCGGTCCCGCGCGCTCATCGCT 480

QY 1509 GTGCTCTGGCGCGTGGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 1568  
DB 481 GTGCTCTGGCGCGTGGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 540

QY 1569 CAGGACCCCGCATCTCCGTAGTCCGGGCGCTCAATGGCACCGCGCGATCGCTTCTCG 1628  
DB 541 CAGGACCCCGCATCTCCGTAGTCCGGGCGCTCAATGGCACCGCGCGATCGCTTCTCG 600

QY 1629 CCTCTGCGCTGTGCGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 1688  
DB 601 CCTCTGCGCTGTGCGCGCTGTCTGCGCGTCCCTTCTTCTGTTGGGGGTGCGAG 660

QY 1689 GGGCCCGAGACCGCGAGCGCGCGGTGTTGAGCGGAAATGCGGCGGAGCCCGCG 1748  
DB 661 GGGCCCGAGACCGCGAGCGCGCGGTGTTGAGCGGAAATGCGGCGGAGCCCGCG 720

QY 1749 CAGCTGGGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1808  
DB 721 CAGCTGGGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780

QY 1809 CTGTGCTCAGCATCTCTACCGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCG 1868  
DB 781 CTGTGCTCAGCATCTCTACCGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCG 840

QY 1869 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGCGCAACCGCGAGCGTCCGCGTCTG 1928  
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1929 C 1929  
901 C 901

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Db 721 CAGCTGGCGCGCTGCGTGTCTATGCTGGGGTACCAACCGCTACTTCTTCTGCGCCCTTT 780
Qy 1809 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGC 1868
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGC 840
Qy 1869 CTGGAGGCGCGCGCGCTCTGGGGCGGAGAGAGGCAACCGGACAGCGTCCGGTCTGT 1928
Db 841 CTGGAGGCGCGCGCGCTCTGGGGCGGAGAGAGGCAACCGGACAGCGTCCGGTCTGT 900
Qy 1929 C 1929
Db 901 C 901

RESULT 8
US-10-290-078-14
; Sequence 14, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MPI2001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-290-078-14

Query Match 29.4%; Score 901; DB 15; Length 1239;
Best Local Similarity 100.0%; Pred. No. 6.4e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 ATGGGAGCCCTCGAAGCAGGAGCAGCGGCCCGGAGGCGCGGAGCCCGCTGTGGCC 1088
Db 1 ATGGGAGCCCTCGAAGCAGGAGCAGCGGCCCGGAGGCGCGGAGCCCGCTGTGGCC 60
Qy 1089 GCGTGTCCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGTGCGC 1148
Db 61 GCGTGTCCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGTGCGC 120
Qy 1149 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
Db 121 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 1209 ATGTGATTCGGGCGCTACCGGAGCATGCGGACACACCACTTGTACTGGGAGCATG 1268
Db 181 ATGTGATTCGGGCGCTACCGGAGCATGCGGACACACCACTTGTACTGGGAGCATG 240
Qy 1269 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1328
Db 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 1329 TCGGGCGCTCGGTGTTTCGGGCGCGCTGCTGCTGCGCCCTGCTGCTGCTGCTGCTGCT 1388
Db 301 TCGGGCGCTCGGTGTTTCGGGCGCGCTGCTGCTGCGCCCTGCTGCTGCTGCTGCTGCT 360
Qy 1389 TGCACCTACGCCACGCTGCTGACATGACCGGCTCAGCGTTCAGCGGCTACTGCGCCATC 1448
Db 361 TGCACCTACGCCACGCTGCTGACATGACCGGCTCAGCGTTCAGCGGCTACTGCGCCATC 420
Qy 1449 TGCGCGCGCTCCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508
Db 421 TGCGCGCGCTCCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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Qy 1509 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1568
Db 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 1569 CAGGACCCCGGCATCTCCGTAGTCCGGGCTCAATGGACCGCGCGGATCGCTCTGCTG 1628
Db 541 CAGGACCCCGGCATCTCCGTAGTCCGGGCTCAATGGACCGCGCGGATCGCTCTGCTG 600
Qy 1629 CCTCTGCGCTGCTGCGCGCTCTGCTGCTGCTGCGGGCGCCACCGCGCGCTGCTGCT 1688
Db 601 CCTCTGCGCTGCTGCGCGCTCTGCTGCTGCTGCGGGGCGCCACCGCGCGCTGCTGCT 660
Qy 1689 GGGCCCGAGACCGCGGAGCGCGCGCTGTTCAGCGCGCGAATGCGGCGCGAGCCCGCG 1748
Db 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTCAGCGCGCGAATGCGGCGCGAGCCCGCG 720
Qy 1749 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1808
Db 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 1809 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGCG 1868
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGCG 840
Qy 1869 CTGCGAGCGCGCGCGCTCTGGGGCGGAGAGAGGCAACCGGACAGCGTCCGGTCTGT 1928
Db 841 CTGCGAGCGCGCGCGCTCTGGGGCGGAGAGAGGCAACCGGACAGCGTCCGGTCTGT 900
Qy 1929 C 1929
Db 901 C 901

RESULT 9
US-10-206-677-1
; Sequence 1, Application US/10206677
; Publication No. US20030186336A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Kulanter, Bruce G.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO
; TITLE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)
; FILE REFERENCE: 1920-1-8
; CURRENT APPLICATION NUMBER: US/10/206,677
; CURRENT FILING DATE: 2002-11-06
; PRIOR FILING DATE: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 60/250,452
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-206-677-1

Query Match 29.4%; Score 901; DB 16; Length 1239;
Best Local Similarity 100.0%; Pred. No. 6.4e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 ATGGGAGCCCTCGAAGCAGGAGCAGCGGCCCGGAGGCGCGGAGCCCGCTGTGGCC 1088
Db 1 ATGGGAGCCCTCGAAGCAGGAGCAGCGGCCCGGAGGCGCGGAGCCCGCTGTGGCC 60
Qy 1089 GCGTGTCCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGTGCGC 1148
Db 61 GCGTGTCCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGTGCGC 120
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Query Match	24.8%;	Score 761.4;	DB 19;	Length 1179;
Best Local Similarity	77.9%;	Pred. No. 8.e-176;		
Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;				
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Dd	1	CAAAATCCCTTCGAAAATACCGGAAATAACCAAATACAAAAACGCCCGTACAATACTCTCAA	60	



Db 579 AACGACACGTAATAACCGTAATTAATCGAACCGTACCGAAACATACGAAACCAACCACC 520  
Qy 1248 AACTTGTACCTGGGCGAGCATGGCGGTGTCCGACCTACTCATCTCTGCTGGGCTGCGGTTTC 1307  
Db 519 AACTTATACCTAAACAAATACCGTATCCGACCTACTCATCTCTACTCGAACTACCGTTTC 460  
Qy 1308 GACCTGTACCGCTCTTGGCGCTTCGGGCGCTTGGGTGTTTCGGGCGCTGCTCTGCGGCTG 1367  
Db 459 GACCTATACCGCTCTTACCGCTTCGCGACCTTAATAATTCGAACCGCTACTCTACCGCTA 400  
Qy 1368 TCCCTCTACGTGGGCGAGGCTGCACCTACCGCAGCTGCTGCACATGACCGCGCTCAGC 1427  
Db 399 TCCCTCTACGTAAACGAAACTACACCTACCGCAGCTACTACACATAACCGCGCTCAAC 340  
Qy 1428 GTCGAGGCTACCTGGCCATCTGCGCGCTGCTCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 1487  
Db 339 GTCGACGCTACCTAACCATCTACCGCGCTTCCGCGCGCTGCTTAACTACCGGAGC 280  
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Db 279 CGGTTCGCGCGCTCATCGCTATATCTTAAACCGTAACCGCTACTCTTACCGATCCCTTC 220  
Qy 1548 TTGTTCTGTGGGCTGCGAGGACCGCGGCTCTCCGTAGTCCGCGGCTCAATGGC 1607  
Db 219 TTAATCTCTAAACGCTGAAACAAACCCGACATCTCCGTAATCCCGAACTCAATAAC 160  
Qy 1608 ACCGCGGAGTGGCTCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1667  
Db 159 ACCGCGGAGTGGCTCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 100  
Qy 1668 CCACCGCGCTCCCGCGCTGCGGCGCGGAGACCGCGGAGCGCGGCGCTGTTTCAAGCGC 1727  
Db 99 CCACCGCGCTCCCGCGCTGCGGCGCGGAGACCGCGGAGACCGCGGAGCTATTCAACCGC 40  
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RESULT 14  
US-10-363-483A-33738  
; Sequence 33738, Application US/10363483A  
; Publication No. US20050064401A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain  
; TITLE OF INVENTION: illnesses  
; FILE REFERENCE: 82011  
; CURRENT APPLICATION NUMBER: US/10/363,483A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 33738  
; LENGTH: 1179  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: Cpg-Island No: 33738  
US-10-363-483A-33738

Query Match 24.8%; Score 761.4; DB 19; Length 1179;  
Best Local Similarity 77.9%; Pred. No. 8.8e-176;  
Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

Qy 588 CAGATCCCTTCGAAGGTCCCGGAGTACAGACTGACAAAACGCGCGTACAGTGTCTCAG 647  
Db 1 CAATCCCTTCGAAAATACCGGAAATACCAAACTAAACAAAACGCGGTACAACTCA 60  
Qy 648 TCCTGTAAACAAAGCTGTCTAGGTGAGACATGCTCACCAGGACCGGCTAGGCTGTGT 707  
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Qy 708 CGCTAAGGCGCGCGGTATTCCAGTTAGTGAGAGGGAAGCGCCCTTGAACTGCATGCGC 767  
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Qy 888 GCCCGCAGCGCAGCGCAGCGCTCCGCGCTGTGACCTGCGCGCGCGCGAGCGTTCGGGCT 947  
Db 301 GCCCGCAACGCAACCAACGCTCCGCGCTTAACTACCGCGCGCGCGCAAGTACGAACT 360  
Qy 948 GGGNAAGGAGCGCTCACCGAGAGGAGCACCGCGCAGGCTCCAGCGCCGAGCGCGGAGC 1007  
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Db 421 CGAGCAGCGCGGAAACACCCATNAACACCCCTAAACGAAACGAGACCGCGCCGAAAAA 480  
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Qy 1188 AGCGGCAACGTGTGACCGGTGATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACACC 1247  
Db 601 AACGACAACTGTAACCGTAATTAATCGAACGCTACCGAAACATACGAAACCAACACC 660  
Qy 1248 AACTTGTACCTGGGCGAGCATGGCGGTGCTGCGACCTACTCATCTGCTGCGGCTGCGGTT 1307  
Db 661 AACTTATACCTAAACAACTAACCGTATCGGACCTACTCATCTCTCTGAACTACCGTTT 720  
Qy 1308 GACCTGTACCGCTCTGCGCGCTGCGCGCGCTGGGTGTTGGGCGCGCTGCTGCGCGCTG 1367  
Db 721 GACCTATACCGCTCTAACGCTCGGACCCCTTAAATTTTCGAAACGCTACTCTACCGCTA 780  
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Db 781 TCCCTCTACGTAAACGAAACTACACCTAGCCAGCTACTACACATAACCGCGCTCAAC 840  
Qy 1428 GTCGAGCGCTACCTGGCCATCTGCGCGCGCTGCGCGCGCGCTTGGTTCACCGCGCGC 1487  
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Db 1021 ACCGCGGATCGCTCTCTCGCTCTGCGCTGCTGCGCGCTCTCTAACTCTCGCGAGC 1080  
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Db 1081 CCACCGCGCTCCCGCGCTGAAACCGGAAACCGGAAACCGGAGCGCTATTCAACCGC 1140  
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US-10-363-345A-33739  
; Sequence 33739, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 33739  
; LENGTH: 1179  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: Cpg-island No: 33739  
US-10-363-345A-33739

Query Match 23.5%; Score 722; DB 18; Length 1179;  
Best Local Similarity 75.8%; Pred. No. 3.8e-166;  
Matches 893; Conservative 0; Mismatches 285; Indels 0; Gaps 0;  
QY 589 AGATCCCTTCGAAGTGCCTGGAGTACCGAGTACGACACTGACAAAGCGCCGCTACAGTGTCTAGT 648  
DB 2 AGATTTTTCGAAGGTGTTCCGAGTATTAGATTGATAAAGCGTTCGTATAGTGTAGT 61  
QY 649 CCGTGAACCAAGCTGTCTAGGTGCAGACATCGTCTACCGGACCGGTAGGCTCGTGC 708  
DB 62 TTGTGAATTAAGTGTCTAGGTTGTAGATTCGTTTATCGGATCGGGTTCGTGC 121  
QY 709 GCTAAGGCGCGCGGTATTTCAGTTAGTGGAGAGGAGCGCCCTGGAACTGCATGGGCC 768  
DB 122 GTTAGGGCGTCCGGTATTTTAGTTAGTGGAGAGGAGCGTTTGGAAATGTATGGGT 181  
QY 769 CGGAGAGGCGCGCGGAGCGGAGCATGCGCGGCGCGGCGCGGCGCGCGCGCGCGCGG 828  
DB 182 CGGAGAGGCGCGCGGAGCGGAGTAGGTTCGGGTTCGGGCGCGGTTCGGGCGGA 241  
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DB 362 GGAAGGAGGCGCTTATCGAGAGGATTAACGCGTTAGGTTTATAGTTTCGATTCGAGCGC 421  
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DB 1142 AATCGCGTTCGAGTTTCGCGTAGTTGGCGCGCTTCGCT 1179

Search completed: April 11, 2005, 21:00:19  
Job time : 1795.07 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:20 ; Search time 12160.1 Seconds  
(without alignments)  
9597.380 Million cell updates/sec

Title: US-09-719-485-1  
Perfect score: 3066  
Sequence: 1 ttgaattatctgtcactg.....acgtgaagacgtggataa 3066

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	693.8	22.6	843	5	BUS53576
2	576	18.8	590	2	BF513101 UI-H-BW1-
3	509	16.6	509	7	CR747135 CR747135
4	490.2	16.0	495	2	BF512085 UI-H-BW1-
5	360.6	11.8	399	8	AQ939773 NR5-116R
6	255.8	8.3	425	8	AQ138681 HS_3073 A
7	231.6	7.6	1046	9	AY407666 Mus muscu
8	230.4	7.5	688	7	CO959476 AGENCOURT
9	230	7.5	4435	3	AK049671 Mus muscu
10	227.8	7.4	640	6	CD618070 56030361H
11	227.8	7.4	640	6	CD618071 56030361J
12	227.8	7.4	1052	9	AY407664 Homo sapi
13	226.8	7.4	500	2	BF603623 269181 MA
14	225.2	7.3	637	6	CD618076 56030461H
15	219.2	7.1	608	6	BY724644 BY724644
16	213.2	7.0	969	9	AY407665 Pan trogl
17	204	6.7	370	5	BX485214 DKF2p686E
18	203.8	6.6	635	6	CD618069 56030353J
19	202.2	6.6	576	6	CD618067 56030345J
20	200.8	6.5	489	1	AL042230 DKF2p434I
21	198.2	6.5	2669	3	BC035179 Homo sapi
22	197.8	6.5	606	5	BQ778458 1131d07.x
23	197.8	6.5	619	5	BX505458 DKF2p686E
24	197.8	6.5	712	6	CD246087 AGENCOURT

25	197.8	6.5	721	6	CD364665
26	197.8	6.5	722	7	CN263776
27	197.8	6.5	779	6	CA442904
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29	196.8	6.4	639	5	BM992802
30	196.6	6.4	391	1	AI569401
31	196.2	6.4	656	6	CA420015
32	196	6.4	741	9	AG113248
33	196	6.4	3204	3	HSM804305
34	195.2	6.4	337	5	BUS566980
35	194.8	6.4	457	2	BF939646
36	193.6	6.3	416	6	CD520893
37	193.4	6.3	353	1	AV657198
38	193.4	6.3	854	8	AQ747659
39	193.2	6.3	643	6	CD618077
40	193	6.3	537	8	AQ322719
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#### ALIGNMENTS

RESULT 1  
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DEFINITION AGENCOURT\_10242213 NIH\_MGC\_109 Homo sapiens cDNA clone IMAGE:6577973 5', mRNA sequence.  
ACCESSION BUS53576  
VERSION BUS53576.1 GI:22903848  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCES  
1 (Bases 1 to 843)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CM2778 row: p column: 05  
High quality sequence stop: 534.  
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/note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

#### FEATURES

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#### ORIGIN

Query Match 22.6% Score 693.8; DB 5; Length 843;



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DB 181 GCTCCCTTTCTTATTTTCAGTTCACAGCTCCACCCCGGTAATCCCAATCCCGAGAAA 240
QY 2101 ACCATGTCCTGTCCTCCAGGAGCTCTGGGGACCCACAGGGCGCTTTGAGGGTGGATCCC 2160
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QY 2281 TTGAGAACAGCAGGAGATTCATTAAAGCTAAATTTTTTTTAAATGTTAAAGTATGATGCT 2340
DB 421 TTGAGAACAGCAGGAGATTCATTAAAGCTAAATTTTTTTTAAATGTTAAAGTATGATGCT 480
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DB 481 GAAGCTAAAGTAAACCTTGTCTGATCAAAAAGTAAAGATTTGTGCAGACCTGTTGTAGA 540
QY 2401 ATTCTTTTCAACAGAGACAGAAAACCTTGTCTCCGAATGGGTTGTGGA 2450
DB 541 ATTCTTTTCAACAGAGACAGAAAACCTTGTCTCCGAATGGGTTGTGGA 590

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## RESULT 3

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CR747135/c
LOCUS CR747135 NCI CGAP Sub7 Homo sapiens mRNA linear EST 30-AUG-2004
DEFINITION IMAGE:3070549 5', mRNA sequence.
ACCESSION CR747135
VERSION CR747135.1 GI:51660528
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE 1 (bases 1 to 509)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,B.,
Peters,M., Radelof,U. and Schneider,D.
TITLE I.M.A.G.E. cDNA Clone Collection
JOURNAL Unpublished (2004)
COMMENT Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: IMGP9981147713.
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Ariart

```

```

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel.: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.
Location/Qualifiers
1. 509
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub7"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP Sub7
is a subtracted library derived from NCI CGAP Sub6."

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## ORIGIN

```

Query Match 16.6%; Score 509; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 3 4e-69;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2255 ACAATGAGGAGTCTCACAGTGTCTTGAGAACAGCAGGAGATTTTCATTAAGCTAAAA 2314
DB 509 ACAATGAGGAGTCTCACAGTGTCTTGAGAACAGCAGGAGATTTTCATTAAGCTAAAA 450
QY 2315 TTTTATTTAATGTTAAAGTATGCTGAGCTAAAGCTAAAGCTGCTGATCAAAAAG 2374
DB 449 TTTTATTTAATGTTAAAGTATGCTGAGCTAAAGCTAAAGCTGCTGATCAAAAAG 390
QY 2375 TAAAGATTGTGCAGACCTGTTGTAGAATTCCTTTCAACAGAGAACAGAAAACTGTCTCC 2434
DB 389 TAAAGATTGTGCAGACCTGTTGTAGAATTCCTTTCAACAGAGAACAGAAAACTGTCTCC 330
QY 2435 GAAGTGGGTTTGTGGAAGAGCCTGCCAAGCGGCTTGTTCAGAGAAATTTGCTCTCTCT 2494
DB 329 GAAGTGGGTTTGTGGAAGAGCCTGCCAAGCGGCTTGTTCAGAGAAATTTGCTCTCTCT 270
QY 2495 GGTATATGTCAGCCTTGATTAACATATGGAGCCTACTATGCAAGTTTAAAGCAAGTA 2554
DB 269 GGTATATGTCAGCCTTGATTAACATATGGAGCCTACTATGCAAGTTTAAAGCAAGTA 210
QY 2555 TCCATGAGCCTGCAGCCTGCTGCTCAATTTTCTGGGGTGAGGATCTGCCCTAGTAGAAGTT 2614
DB 209 TCCATGAGCCTGCAGCCTGCTGCTCAATTTTCTGGGGTGAGGATCTGCCCTAGTAGAAGTT 150
QY 2615 TTCTCTAATTTTAAATTTTGTCTGTTACTTGTATTTAGATGTTTCTTGTGCGGGGTGGGGG 2674
DB 149 TTCTCTAATTTTAAATTTTGTCTGTTACTTGTATTTAGATGTTTCTTGTGCGGGGTGGGGG 90
QY 2675 TTTATTTGCTTCCCAATGCTTTTGTAAATCCCGGTGCTGTGCTCTATGTTGTCAGTGGTGG 2734
DB 89 TTTATTTGCTTCCCAATGCTTTTGTAAATCCCGGTGCTGTGCTCTATGTTGTCAGTGGTGG 30
QY 2735 TGGTTCCTGGCATTATTAATTTGCTGGTTG 2763
DB 29 TGGTTCCTGGCATTATTAATTTGCTGGTTG 1

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NCI CGAP Sub7 library had 12 million recombinants. A single-stranded DNA preparation of NCI CGAP Sub6 was used as a tracer in a subtractive hybridization with a driver comprising the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones 1323278-1323911, 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI CGAP Lys pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI CGAP Br22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clones 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clones 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clones 2710536-2712455) (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clones 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clones 2723592-2729346) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP Sub6 (IMAGE Clones 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806."





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/organism="Homo sapiens"
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ORIGIN
Query Match      11.8%; Score 360.6; DB 8; Length 399;
Best Local Similarity 96.2%; Pred. No. 3.9e-46;
Matches 380; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 624 CAAAGCCCGCTACAGTCTCAGTCTGTAAACCAAGCTGTCTAGGCTGAGACATCGC 683
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QY 684 TCACCGGACCGGTAGGCTCTGTCGCTAAGGGCGCGGGTA-TTCCAGTTAGTGGAG 742
DB 335 TCACCGGACCGGTAGGCTCTGTCGCTAAGGGCGCGGGTATTTCAGTTAGTGAAG 276
QY 743 GGAAGCCCGCTGGAACCTGATGGCGCGGAGAGGGCGCGGAGCATGCGCGGC 802
DB 275 GGAAGCCCGCTGGAACCTGATGGCGCGGAGAGGGCGCGGAAACGGAGCGCGGC 216
QY 803 CGGGCGCGCGCGCGCTGCGCGAGACTGCGCGAGCTAGCTCGGAGCGCTCGGAG 862
DB 215 CGGGCGCGCGCGCGCTGCGCGAGACTTGGCGAGCTAGCTCGGAGCGCTCGGAG 156
QY 863 CCCACCCCGCAGAGCGCTTCTCGCGCCCGCAGCGCAGCGCTCCCGCGCTGAC 922
DB 155 CCCACCCCGCAGAGCGCTTCTCGCGCCCGCAGCGCAGCGCTCCCGCGCTGAC 96
QY 923 CTGCGCGCGCGCAGCGCTGCGCGTGGGAAAGAGGCGCTCACCAGAGGACCAACGCGC 982
DB 95 CTGCGCGCGCGCAGCGCTGCGCGTGGGAAAGAGGCGCTCACCAGAGGACCAACGCGC 36
QY 983 CAGGCTCCAGCCGACCGCGGAGCGCGCGCGC 1017
DB 35 CAGGCTCCAGCCGACCGCGGAGCGCGCGCGC 1

RESULT 6
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LOCUS
DEFINITION HS_3073_A2_D02_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3073 Col=4 Row=G, genomic survey
sequence.
ACCESSION A0138681
VERSION A0138681.1 GI:3529334
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 425)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3073 row: G column: 4
Class: BAC ends
High quality sequence stop: 425.
Location/Qualifiers

FEATURES
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1..425
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Best Local Similarity 94.2%; Pred. No. 7.1e-30;
Matches 274; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 2397 TAGAATCTCTTTCAACAGAGAAACAACTTGTCTCCGAAGTGGGTTTGTGAAGGAAG 2456
DB 51 TCGAATCTCTTTCAACAGAGAAACAACTTGTCTCCGAAGTGGGTTTGTGAAGGAAG 110
QY 2457 CCTGCCAAGCGGCTTGTTCAGAGAAATGCTCTCTCTGTTTATGTCACGCTTGATAA 2516
DB 111 CCTGCCAAGCGGCTTGTTCAGAGAAATGCTCTCTCTGTTTATGTCACGCTTGATAA 170
QY 2517 CACATATGGGAGCTACTATGACGTTTAAAGCAAGTATCCATCAGCTCGAGCTCGT 2576
DB 171 CACATATGGGAGCTACTATGACGTTTAAAGCAAGTATCCATCAGCTCGAGCTCGT 230
QY 2577 CATTTTCTGGGCTGAGGATCTCCCTAGGTAGAGATTTTCTTAATTTATTTGCTGTT 2636
DB 231 CATTTTCTGGGCTGAGGATCTCCCTAGGTAGAGATTTTCTTAATTTATTTGCTG-T 289
QY 2637 ACTTGTATTGACAGTCTTCTGTCGGGTGGGGTGTATTGCTTCC 2687
DB 290 ACTTGTATTGACAGTCTTCTGTCGGGTGGGGTGTATTGCTTCCC 340

RESULT 7
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LOCUS
DEFINITION Mus musculus GHSR gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION A0407666
VERSION A0407666.1 GI:39763637
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1046)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1046)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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## ORIGIN

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Matches 316; Conservative	0; Mismatches 147; Indels 0; Gaps 0;
1121	GCCTTTTCCCTCGGGGCGCTGTGTCCGGGTGACCGTGTGTGCTGTGCTGTTCGTTCGT 1180
Db	 GCTCTTCCCGCGCGCTGTGTGGGGCGGTCAAGCCACCTGCGTGGCACTCTTCGTGGT 118
1181	CGGGGTGAGCGGCAACGTGTGTGACCGTGTATGCTGATCGGGCGCTTACCGGACATCGGGAC 1240
Db	 GGGTATCGCTGGCAACCTGTCTCAACATGCTGTGGTGTGTGCGGTTCGCGAGCTGGGCAC 178
1241	CACACCAACTGTACTCTGGGACGATGGCGGTGTCCGACCTACTCATCTCTGCTCGGGCT 1300
Db	 CACCACCAACTCTACTGTCCAGCATGGCTCTTCGGATCTGCTCATCTCTCTGCAAT 238
1301	GCGGTCGACCTGTACCGCTCTGTGGCGCTCGCGGCCCTGTGGGTGTGGGGCGCTGCTCTG 1360
Db	 GCCCTTGGACCTCGTTTGCCTCTGGCAGTACCGGCCCTTGGAACTTCGCGACCTCCTCTG 298
1361	CGCCCTGTCCCTCTACGTGGCGAGGCGCTGCACCTACGCCACGCTGCTGCACATGACCGC 1420
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1421	GCTCAGCGTCGAGCGCTACTGTGCCCATCTGCCCGCCCGCTCCCGCGCGCGCTCTTGCTCAC 1480
Db	 GCTGAGCGTCGAGCGCTACTTCCGCATCTGCTTCCCACTCCGGGCCAAAGTGGTGGTCCAC 418
1481	CCGGCGCGCGTCCGGCGCTCATCGTGTGCTCTGGGGCGTGGCGCTGCTCTCTGCCGG 1540
Db	 CAAGGGCGCGGTGAAGCTGTGTCACTTCGTCACTTGGGGCGTGGCTTCTGACAGCGCCGG 478
1541	TCCTCTTTGTTTCTGTGGGCGTCGACGAGGACCCCGGCATC 1583
Db	 GCCCATCTTCGTGTCTAGTCCGGGTGGAGCAGGAGACGGCACC 521

RESULT 13  
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LOCUS  
BF603623 500 bp mRNA linear EST 25-APR-2001  
DEFINITION  
269181 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BF603623				
BF603623.1	GI:11701421			
EST.				
Bos taurus			(cow)	
Bos taurus				Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1. (bases 1 to 500)

REFERENCE  
AUTHORS  
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Casas, E., Wray, J.E., White, J., Cho, J., Fahrner, S.C.,  
Bennett, G.L., Heaton, M.P., Maegreid, W.W., Rohrer, G.A.,  
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,  
Quackenbush, J. and Keele, J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4): 626-630 (2001)

TITLE  
JOURNAL

MEDLINE PUBMED	COMMENT
21180013 11282978	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clifty Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers  
 FORWARD: AGGAACACGCTATGACCAT  
 BACKWARD: GTTTCACGACGACGAGC  
 Plate: 49 row: I column: 6  
 Seq primer: ATTAGTGACACTATAG.  
 Location/Qualifiers  
 source 1..500

## FEATURES

## ORIGIN

Query Match	7.4%;	Score 226.8;	DB 2;	Length 500;
Best Local Similarity	68.2%;	Pred. No. 2.2e-25;		
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QY	1120	CGCCCTTTCCCTCGGGGGCGCTGGTCCGGTGACCCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGTGC	1179	
DB	39	CCCTCTTCCCGCGCGCTGTCTGGCGGGCGTCACAGCCACCTGCGTGGCGCTCTTCGTGG	98	
QY	1180	TGGGGGTGAGCGGCAACGTTGGTGACCGGTGATCGGTGATCGGGCGCTACCGGGACATCGCGGA	1239	
DB	99	TGGGCATCGCGGGCAACCTGCTCACCATGTGTGTGTGTGCGGTCTTCGCGAGCTCGGTA	158	
QY	1240	CCACCACCAACTTGTACCTCGGGGAGCATGGCGGTGCCACCTTACCTCATCTCTCTCGGGC	1299	
DB	159	CCACCAACCAACTCTACCTGTCCAGCATGGCGCTTCTCCGACTTACTCATCTTCTCTGCA	218	
QY	1300	TGCGGTTCCAGCTGTATACCGCTCTGTGCGGTTCGCGGCCCTGGGGTTCGGGCGCGCTGCTCT	1359	
DB	219	TGCCCCCTCGACCTCGTGTGCGCTCTGGCAATTACCGGCCCTGGAACTTTGGGCGACCTGCTCT	278	
QY	1360	GCGCCTGTCCCTCTACGTGGGGGAGGGGTGCACCTACGCCAGCGTGTGCACATGACCG	1419	
DB	279	GCAACTCTTCCAGTTTGTACGGGAGAGTGTCACTTACGCTACGCTGCTCACCATCACCG	338	
QY	1420	CGCTCAGGCTCGAGCGCTACCTGGCCATCTGCGGCCCGCTCGCGGCCCGCGTCTTGCTCA	1479	
DB	339	CGTGAAGCGTTCGAGCGCTACTTCCGCCATCTGCTTCCCGCTCGGGGCAAGGTGGTGATCA	398	
QY	1480	CCGGCGCGCGTCCCGCGGCTCATCGCTGTGCTCTTGGGCGGTGGCGGCTGCTCTCTGCCG	1539	
DB	399	CCAAGGGCGGGTGAAGAGTCGTTCATCTGTGTCACTTGGGCGTGGGCTTCTGAGCGCCG	458	
QY	1540	GTCCCTCTTGTTCCTGGTGGGCGTCCAGCAGGACCCCGCA	1591	
DB	459	GGCCCACTCTCGTGTCTGGTTCGAGTGGGACATGAGAATGGCA	500	

RESULT 14  
 CD618076/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 637)  
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 Comment: Fu GK

FEATURES source

Primed with a primer [5'  
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 10.0 and subtraction to Rot = 459.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGATCTCGAGTTAATTAATCCCCCCCCCCC  
3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
modified phagescript KS(+) after bulk excision from Lambda  
FLC I."

## ORIGIN

Query Match	7.1%	Score 219.2;	DB 6;	Length 608;
Best Local Similarity	70.3%	Pred. No. 3.1e-24;		
Matches 293;	Conservative 0;	Mismatches 124;	Indels 0;	Gaps 0;
Qy	1165	TGTGCTGTTGCTGCGGTGAGCGGACACGTTGGTACCGCTGATCGTATCGGGCGCT	1224	
Db	2	TGGCGCTCTTCTGTTGGTGGCATCTCGGGCAACCTGCTCACCATGCTGGTGGTCCCGCT	61	
Qy	1225	ACCGGACATCGGACACCAACCACTTGTACCTGGGAGCATGGCCGCTGTCGACCTAC	1284	
Db	62	TCCGGAGCTGGGACACCAACCACTTACCTATCCAGCATGGCCTTCTCCGATCTGC	121	
Qy	1285	TCATCTGCTCGGGTGCCTGTTGACCTGTACCGCTCTGGCGCTCGCGGCCCTGGGTGT	1344	
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Qy	1345	TGGGCGCGCTGCTGCGCGCTGTCCCTCTAGTGGGAGGGTGCACCTACGCCACGC	1404	
Db	182	TCGGCGACCTGCTCTGCAAACTCTTCCAGTTGTACGCGAGAGCTGCACCTACGCCACGG	241	
Qy	1405	TGCTGCATGACCGCGCTCAGCGTCGAGCGCTACCTGGCCATCTGCCGCCGCTCCGCG	1464	
Db	242	TCCTCACCATCACCGCGTGAAGCTCGAGCGCTACTTCGCCATCTGCTTCCGCTGCGG	301	
Qy	1465	CCCGCGTCTTGGTACACCGCGCGCGCTCCGCGCGCTCATCGCTGTGCTTGGGCGGTGG	1524	
Db	302	CCAGGTGGTGGTCAACCAAGGCGGTGTGAAGCTGTCATCTTGTCTTTGGGCGGTGG	361	
Qy	1525	CGCTGCTCTTGGCGGTCTCTTGTTCCTGGTGGGCGTGCAGCAGACCCCGGCA	1581	
Db	362	CCTTCTGAGCGCGGGGCCATCTTCNTGCTGGTGGGCGTGGAGCAGCAACCGCA	418	

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Job time : 12166.1 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:44:49 ; Search time 662.25 Seconds  
(without alignments)  
11075.206 Million cell updates/sec

Title: US-09-719-485-2

Perfect score: 1239

Sequence: 1 atgggcagccctcggaacgg.....acgtgaagacatgggataa 1239

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	1239	3	Aaz45403 cDNA enco
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3	1239	100.0	1239	4	Aaf85449 Nucleotid
4	1239	100.0	1239	6	Abk90132 DNA enco
5	1239	100.0	1239	8	Abz42842 Human mot
6	1239	100.0	1239	12	Adn11760 Human mot
7	1239	100.0	1239	12	Ado30072 Human GPC
8	1239	100.0	1239	12	Adq37920 Human G-p
9	1239	100.0	1506	4	Aai66989 Human GPR
10	1078	87.0	1390	3	Aaz45404 cDNA enco
11	915.6	73.9	1203	4	Aaf85448 Nucleotid
12	901	72.7	1161	4	Aaf83684 Short for
13	901	72.7	1161	12	Adn11762 Human mot
14	901	72.7	3066	3	Aaz45402 Genomic s
15	901	72.7	110000	10	Adg70447 Human ANG
16	901	72.7	110000	10	Abz79565 CLLD8 and
17	896.2	72.3	2040	3	Aaa46116 Human G p
18	896.2	72.3	2040	12	Adg86490 Human ngp
19	896.2	72.3	2040	12	Adp20283 Human GPC
20	891.4	71.9	2040	12	Adg86512 Human orp

21	546	44.1	813	4	Aaf85447 Nucleotid
c	501.2	40.5	1179	6	Abq47146 Oligonucl
23	501.2	40.5	1179	6	Abq47147 Oligonucl
c	437.2	35.3	1179	6	Abq47149 Oligonucl
25	437.2	35.3	1179	6	Abq47148 Oligonucl
26	283	22.8	283	2	Aav28290 Galanin r
27	283	22.8	283	2	AAV32651 Galanin r
28	283	22.8	283	2	Aav44930 Galanin r
29	283	22.8	283	2	ABK14060 Rat galan
30	264.8	21.4	1092	3	Aaz45405 DNA enco
31	264.8	21.4	1092	4	Aaf85450 Nucleotid
32	255.8	20.6	1050	3	Aaz61492 cDNA enco
33	234.8	19.0	1063	2	AAZ69754 Swine gro
34	234.8	19.0	1063	2	AAT68662 Pig growt
35	233.2	18.8	1029	2	AAT69755 Swine gro
36	233.2	18.8	1029	2	AAT68663 Pig growt
37	231.6	18.7	1095	3	Aaz45593 cDNA enco
38	231.6	18.7	4009	3	AAZ45967 DNA enco
39	230	18.6	1092	12	ADO29027 Mouse nov
40	229.8	18.5	1092	4	AAH27800 Rat growt
41	229	18.5	250	10	ACA55761 Pig signa
42	229	18.5	250	12	ADI55557 Human pol
43	228.8	18.5	870	8	ABz42674 Human gro
44	228.8	18.5	1122	2	AAT68665 Human gro
45	228.4	18.4	3129	2	AAT69759 Rat growt

ALIGNMENTS

RESULT 1

AAZ45403  
ID AAZ45403 standard; cDNA; 1239 BP.

XX AAZ45403;

DT 27-MAR-2000 (first entry)

DE cDNA encoding the motilin receptor splice variant MTL-RIA.

XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;  
KW spliced form; MTL-RIA; MTL-R1B; gastric motility disorder;  
KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;  
KW infection; stress-related motility disorder; psychogenic disorder;  
KW gastroparesis; gastro-oesophageal reflux disease; constipation;  
KW chronic idiopathic pseudo obstruction; acute faecal impaction;  
KW postoperative ileus; gallstones; infantile colic; diarrhoea;  
KW irritable bowel syndrome; non-ulcer dyspepsion; non-cardiac chest pain;  
XX endoscopy; duodenal intubation; ds.

OS Homo sapiens.

XX Key Location/Qualifiers  
CDS 1..1239  
/\*tag= a  
/product= "MTL-RIA"

PN WO9964436-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012773.

XX 12-JUN-1998; 98US-0089098P.

XX (MERI ) MERCK & CO INC.

XX Feighner SD, Patchett AA, Tan C, Mckee K, Macneil D, Howard AD;  
PI Pong S, Smith RG;  
XX WPI; 2000-105868/09.  
DR P-PSDB; AAY54145.

XX Novel receptor protein for screening compounds used in treating irritable  
PT bowel syndrome, constipation and other gastric conditions.  
XX Claim 4; Fig 2; 44pp; English.  
XX The present sequence encodes splice variant MTL-R1A of the motilin  
CC receptor. The gene encodes a G-protein coupled receptor, and is  
CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A  
CC (see AY54145) and MTL-R1B (see AY54146). MTL-R1A is a functional seven  
CC transmembrane domain form, and MTL-R1B is a truncated five transmembrane  
CC domain. The MTL-R1 proteins are used to identify agonists and antagonists  
CC which can be used for treating gastric motility disorders, functional  
CC defects, disorders secondary to neurological disorders e.g. scleroderma,  
CC paraneoplastic syndromes radiation induced dysmotility, diabetes,  
CC infections, stress-related motility disorders, psychogenic disorders,  
CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic  
CC idiopathic pseudo obstruction, acute faecal impaction, postoperative  
CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer  
CC dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used  
CC in the preparation for colonoscopy, endoscopy and duodenal intubation  
XX  
SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1239; DB 3; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 3e-215;  
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAGCCCTGTGAACGGCAGCAGCGCCCGAGGGGGCGCGGAGCGCGCGTGGGCC 60  
DB 1 ATGGCAGCCCTGTGAACGGCAGCAGCGCCCGAGGGGGCGCGGAGCGCGCGTGGGCC 60  
QY 61 GGGCTGCCGCTTGGCAGAGCGCCGCTGCTGCCCTTTCCCTGGGGCGCGTGGTGGCG 120  
DB 61 GGGCTGCCGCTTGGCAGAGCGCCGCTGCTGCCCTTTCCCTGGGGCGCGTGGTGGCG 120  
QY 121 GTGACCGCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
DB 121 GTGACCGCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
QY 181 ATGCTGATCGGGCGCTACGGGACATGGGACACACCACTTGTACTTGGGCGAGCATG 240  
DB 181 ATGCTGATCGGGCGCTACGGGACATGGGACACACCACTTGTACTTGGGCGAGCATG 240  
QY 241 GCGGTGTGCGACCTACTCATCTGCTCGGGCTCGCGCTTGCACCTGTACCGCTCTGGCGC 300  
DB 241 GCGGTGTGCGACCTACTCATCTGCTCGGGCTCGCGCTTGCACCTGTACCGCTCTGGCGC 300  
QY 301 TCGCGCCCTGTGGTGTGGGCGCTGTGCTGTGCGCCCTGTCCCTCTACGTGGGCGAGGCG 360  
DB 301 TCGCGCCCTGTGGTGTGGGCGCTGTGCTGTGCGCCCTGTCCCTCTACGTGGGCGAGGCG 360  
QY 361 TGCACCTAGCCACGCTGTGCATGACATGACCGGCTCAGGCTCGAGCGCTACTTGGCCATC 420  
DB 361 TGCACCTAGCCACGCTGTGCATGACATGACCGGCTCAGGCTCGAGCGCTACTTGGCCATC 420  
QY 421 TSCCGCGCTCGCGCGCTGTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480  
DB 421 TSCCGCGCTCGCGCGCTGTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480  
QY 481 GTGCTCTGGGCGCTGGCGCTGTCTCTGCGCGTCCCTTTCTTTGCTTCTGCTGGCGCTGAG 540  
DB 481 GTGCTCTGGGCGCTGGCGCTGTCTCTGCGCGTCCCTTTCTTTGCTTCTGCTGGCGCTGAG 540  
QY 541 CAGGACCCCGGATCTCGTAGTCCCGGCGCTCAATGGACCGCGGATGCGCTCTCTCG 600  
DB 541 CAGGACCCCGGATCTCGTAGTCCCGGCGCTCAATGGACCGCGGATGCGCTCTCTCG 600  
QY 601 CCTCTCGCTCGTCCGCGCTCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 660  
DB 601 CCTCTCGCTCGTCCGCGCTCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 660  
QY 661 GGGCCCGAGACCGCGAGGCGCGGCGTGTGTTTACGCCCGAATGCCGCGGAGCCCGCG 720

DB 661 GGGCCCGAGACCGCGAGGCGCGGCGTGTGTTTACGCCCGAATGCCGCGGAGCCCGCG 720  
QY 721 CAGTGGGCGCGTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780  
DB 721 CAGTGGGCGCGTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780  
QY 781 CTGTGCTTCAGCATCTCTACGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCGCG 840  
DB 781 CTGTGCTTCAGCATCTCTACGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCGCG 840  
QY 841 CTGCGAGCCCGCGCGCTCGGGCGGAGAGGCGCACCGGCGAGCGTCCGCGTCTCTG 900  
DB 841 CTGCGAGCCCGCGCGCTCGGGCGGAGAGGCGCACCGGCGAGCGTCCGCGTCTCTG 900  
QY 901 CTGTGCTGGTGTGGCATTTTAAATTTGCTGGTGGCTTCCACGTTGGCAGATCAATT 960  
DB 901 CTGTGCTGGTGTGGCATTTTAAATTTGCTGGTGGCTTCCACGTTGGCAGATCAATT 960  
QY 961 TACATAAACACGGAAGATTTCGGGATGATGTCTCTCAGTACTTTAAACATCTCTGCT 1020  
DB 961 TACATAAACACGGAAGATTTCGGGATGATGTCTCTCAGTACTTTAAACATCTCTGCT 1020  
QY 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTTACAACTCATTTCAAAG 1080  
DB 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTTACAACTCATTTCAAAG 1080  
QY 1081 AAGTACAGAGCGCGCGCTTTTAAATCTGCTGTCTCAGGAAAGTCCAGGCCGAGAGGCTTC 1140  
DB 1081 AAGTACAGAGCGCGCGCTTTTAAATCTGCTGTCTCAGGAAAGTCCAGGCCGAGAGGCTTC 1140  
QY 1141 CACAGAGCAGGAGACACTGCGGGGAAAGTTTCAGGGGACACTGGAGGAGACACGCTGGGC 1200  
DB 1141 CACAGAGCAGGAGACACTGCGGGGAAAGTTTCAGGGGACACTGGAGGAGACACGCTGGGC 1200  
QY 1201 TACACCGAGACAAAGCGCTAACGTGAAGACGATGGGATAA 1239  
DB 1201 TACACCGAGACAAAGCGCTAACGTGAAGACGATGGGATAA 1239  
RESULT 2  
AAP85449 standard; cDNA; 1239 BP.  
XX AC AAP85449;  
XX DT 23-JUL-2001 (first entry)  
XX DE Nucleotide sequence of a human motilin receptor polypeptide.  
XX KW Motilin receptor; gastrointestinal disease; gastric motility disorder;  
XX KW gastroparesis; irritable bowel syndrome; diarrhoea; ss.  
XX OS Homo sapiens.  
XX PH Key Location/Qualifiers  
XX FT CDS 1..1239  
XX FT /\*tag= a  
XX FT /note= "motilin receptor"  
XX WO200132710-A1.  
XX PD 10-MAY-2001.  
XX PF 25-OCT-2000; 2000WO-US029426.  
XX PR 29-OCT-1999; 99US-0162264P.  
XX PA (MERI ) MERCK & CO INC.  
XX PI Tan C, McKee K;  
XX DR WPI; 2001-343479/36.

DR P-PSDB; AAB68478.

XX Novel polypeptides related to dog and rabbit motilin receptor

PT polypeptide, comprising unique regions from dog and motilin receptor

PT amino acid sequence, useful for identifying compounds for treating

PT diarrhea in humans.

XX Disclosure; Page 34; 42pp; English.

XX The present sequence encodes a human motilin receptor polypeptide. The

CC specification describes a unique sequence present in exon 1 of the dog

CC motilin receptor, which is not present in human or Sphaeroides nephelus

CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is

CC useful for measuring the ability of a compound to affect motilin receptor

CC activity. Motilin receptor polynucleotides and polypeptides are used to

CC identify therapeutic compounds and are useful for treating

CC gastrointestinal diseases and disorders such as gastric motility

CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea

XX

SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 100.0%; Score 1239; DB 4; Length 1239;

Best Local Similarity 100.0%; Pred. No. 3e-215;

Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGACGCGCTGGAACGGGACGACGCGCCCGAGGGGGCGGGAGCCCGCTGGGCC 60

Db 1 ATGGGACGCGCTGGAACGGGACGACGCGCCCGAGGGGGCGGGAGCCCGCTGGGCC 60

Qy 61 GCGTGGCGCTTGGGACGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGGTGGCG 120

Db 61 GCGTGGCGCTTGGGACGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGGTGGCG 120

Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Qy 181 ATGCTGATCGGCGCTACCGGACATCGGACACACACCACTTGTACCTGGGCGAGCATG 240

Db 181 ATGCTGATCGGCGCTACCGGACATCGGACACACCACTTGTACCTGGGCGAGCATG 240

Qy 241 GCGGTGCGGACCTACTATCTGCTGGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGG 300

Db 241 GCGGTGCGGACCTACTATCTGCTGGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGG 300

Qy 301 TCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Db 301 TCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Qy 361 TGCACCTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

Db 361 TGCACCTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

Qy 421 TGCACCTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

Db 421 TGCACCTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

Qy 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

Db 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

Qy 541 CAGGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

Db 541 CAGGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

Qy 601 CCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

Db 601 CCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

Qy 661 GGGCCGAGACCGCGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

Db 661 GGGCCGAGACCGCGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

Qy 721 CAGTGGGGCGCGCTGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

Db 721 CAGTGGGGCGCGCTGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

Qy 781 CTGTGCGCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGGAGCAGCGCGCGGCGG 840

Db 781 CTGTGCGCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGGAGCAGCGCGCGGCGG 840

Qy 841 CTGTGAGGCGCGCGCTGCGGCGGGAGAGAGGCGCACCGGAGACCGTCCGCGTCTG 900

Db 841 CTGTGAGGCGCGCGCTGCGGCGGGAGAGAGGCGCACCGGAGACCGTCCGCGTCTG 900

Qy 901 CTGTGTGTGTCTGCGCATTTATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

Db 901 CTGTGTGTGTCTGCGCATTTATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

Qy 961 TACATAAACCGGAGGATTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

Db 961 TACATAAACCGGAGGATTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

Qy 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTTACAACTTCATTTCAAAG 1080

Db 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTTACAACTTCATTTCAAAG 1080

Qy 1081 AAGTACAGAGCGCGGCTTTAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

Db 1081 AAGTACAGAGCGCGGCTTTAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

Qy 1141 CACAGAGCAGGAGACCTGCGGGGAGTTGCGAGGAGACCTGCGAGGAGACACCGTGGGC 1200

Db 1141 CACAGAGCAGGAGACCTGCGGGGAGTTGCGAGGAGACCTGCGAGGAGACACCGTGGGC 1200

Qy 1201 TACACCGGAGCAAGCGCTTAACGTGAGCAGGATGGGATAA 1239

Db 1201 TACACCGGAGCAAGCGCTTAACGTGAGCAGGATGGGATAA 1239

RESULT 3

AAF83683

ID AAF83683 standard; DNA; 1239 BP.

XX AAF83683;

AC AAF83683;

XX 23-JUL-2001 (first entry)

XX Long form of motilin receptor, GPR-38A isoform encoding DNA.

DE zsig33; signal transduction; hormone; enzyme; neural development;

XX gastric contractility; nutrient uptake; digestive; pancreatic; human;

KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;

KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R; ds;

KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.

XX Homo sapiens.

OS Key Location/Qualifiers

XX 1..1239

FT CDS /\*tag= a

FT /product= "GPR-38A"

XX WO200138355-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032074.

XX 22-NOV-1999; 99US-0166765P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI; 2001-355879/37.





psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer; gene; ds.  
XX Homo sapiens.  
XX WO200261087-A2.  
XX 08-AUG-2002.  
XX 19-DEC-2001; 2001WO-US050107.  
XX 19-DEC-2000; 2000US-0257144P.  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX Burner GC, Roush CL, Brown JP;  
XX WPI: 2003-046718/04.  
XX P-PSDB; ABP81993.  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX Disclosure; Fig 1; 523pp; English.  
XX The present invention describes antigenic peptides (I) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. AB242523 to AB242859 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1239; DB 8; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 3e-215;  
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGGAGAGCCCTGGAAAGCGAGCGACGCGCCCGAGGGGGCGCGGAGCGCGCGTGGCCC 60  
DB 1 ATGGGAGAGCCCTGGAAAGCGAGCGACGCGCCCGAGGGGGCGCGGAGCGCGCGTGGCCC 60  
QY 61 GCGCTGCCCTTGGACAGAGCGCGCTGCTCGCCCTTTCCCTTGGGGCGCTGTGTCG 120  
DB 61 GCGCTGCCCTTGGACAGAGCGCGCTGCTCGCCCTTTCCCTTGGGGCGCTGTGTCG 120  
QY 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
DB 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

QY 181 ATGCTGATCGGGCGCTACCGGACATCGGACACCAACCACTTGTACTTGGGAGCATG 240  
DB 181 ATGCTGATCGGGCGCTACCGGACATCGGACACCAACCACTTGTACTTGGGAGCATG 240  
QY 241 GCCGTGTCGACCTACTACTCTCTCGGGTGGCTTGGACCTGTACCGGCTCTGGCGC 300  
DB 241 GCCGTGTCGACCTACTACTCTCTCGGGTGGCTTGGACCTGTACCGGCTCTGGCGC 300  
QY 301 TCGGGCGCTTGGGTGTTTCGGGCGCTGCTCTGCGCGCTGTCCCTCTACCTGGGCGAGGCG 360  
DB 301 TCGGGCGCTTGGGTGTTTCGGGCGCTGCTCTGCGCGCTGTCCCTCTACCTGGGCGAGGCG 360  
QY 361 TGCACCTAGCCACGCTGTCACATGACCGCGCTCAGCGTCTGAGCGCTACCTGGCCATC 420  
DB 361 TGCACCTAGCCACGCTGTCACATGACCGCGCTCAGCGTCTGAGCGCTACCTGGCCATC 420  
QY 421 TCGCGCGCTTGGGTGTTTCGGGCGCTGCTCTGCGCGCTGTCCCTCTACCTGGGCGAGGCG 480  
DB 421 TCGCGCGCTTGGGTGTTTCGGGCGCTGCTCTGCGCGCTGTCCCTCTACCTGGGCGCTCATCGCT 480  
QY 481 GTGCTCTGGGCGCTGCGCGCTGCTCTGCGCGCTGTCCCTCTGTTCTGTTGGTGGGCGTGGAG 540  
DB 481 GTGCTCTGGGCGCTGCGCGCTGCTCTGCGCGCTGTCCCTCTGTTCTGTTGGTGGGCGTGGAG 540  
QY 541 CAGGACCCCGCATCTCCGTAGTCCCGGCTCAATGACCGCGCGATCGCTCTCTCG 600  
DB 541 CAGGACCCCGCATCTCCGTAGTCCCGGCTCAATGACCGCGCGATCGCTCTCTCG 600  
QY 601 CCTCTGCGCTGCTGCGCGCTCTCTGCGCGCTGTCCCTCTGTTCTGTTGGTGGGCGTGGAG 660  
DB 601 CCTCTGCGCTGCTGCGCGCTCTCTGCGCGCTGTCCCTCTGTTCTGTTGGTGGGCGTGGAG 660  
QY 661 GGGCCGAGACCGCGGAGCGCGCTGTTACGCGCGCGATCGCGCGCGAGCGCGCGCG 720  
DB 661 GGGCCGAGACCGCGGAGCGCGCTGTTACGCGCGCGATCGCGCGCGAGCGCGCGCG 720  
QY 721 CAGTGGGCGCGCTGCGGTGCTCATGCTGCTGCTACCGCGCTCTCTCTGCTGCTGCTTT 780  
DB 721 CAGTGGGCGCGCTGCGGTGCTCATGCTGCTGCTACCGCGCTCTCTCTGCTGCTGCTTT 780  
QY 781 CTGTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGGAGCAGCGCGCGCGCG 840  
DB 781 CTGTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGGAGCAGCGCGCGCGCG 840  
QY 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGCGCAGCGTCCGCGTCTG 900  
DB 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGCGCAGCGTCCGCGTCTG 900  
QY 901 CTGCTGCTGCTGCGCATTTATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
DB 901 CTGCTGCTGCTGCGCATTTATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 TACATAACAGGAGATTCGGGATGATGCTCTCTCAGTACTTTAACTCTGCTGCT 1020  
DB 961 TACATAACAGGAGATTCGGGATGATGCTCTCTCAGTACTTTAACTCTGCTGCT 1020  
QY 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080  
DB 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080  
QY 1081 AAGTACAGAGCGCGCGCTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
DB 1081 AAGTACAGAGCGCGCGCTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
QY 1141 CACAGAGCGGAGCATCTCGGGGAGCTTCAGCGGAGCTTCAGGAGAGACACGCTGGG 1200  
DB 1141 CACAGAGCGGAGCATCTCGGGGAGCTTCAGCGGAGCTTCAGGAGAGACACGCTGGG 1200  
QY 1201 TACACCGGAGACAGCGCTTAAAGTGAAGACGATGGGATAA 1239  
DB 1201 TACACCGGAGACAGCGCTTAAAGTGAAGACGATGGGATAA 1239

RESULT 6	
ADN11760	
ID	ADN11760 standard; cDNA; 1239 BP.
XX	
AC	ADN11760;
XX	
DT	15-JUL-2004 (first entry)
XX	
DE	Human motilin receptor GPR-38A coding sequence.
XX	
ss	gene; human; zsig33; body weight; body mass; antibody; antagonist;
KW	gastrointestinal; antiinflammatory; antilulcer; vulnerary;
KW	growth hormone secretagogue; GHS-R; peptide-antibody complex;
KW	motilin receptor.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1239
FT	/*tag= a
FT	/product= "motilin receptor GPR38A"
XX	
PN	WO2004033645-A2.
XX	
PD	22-APR-2004.
XX	
PP	06-OCT-2003; 2003WO-US031804.
XX	
PR	07-OCT-2002; 2002US-0416918P.
XX	
PA	(Zymo ) ZYMOGENETICS INC.
XX	
PI	Jaspers SR., Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
XX	
DR	WPI; 2004-340913/31.
XX	
P-PSDB; ADN11761.	
XX	
PT	Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
PT	inhibiting signal transduction in a cell expressing a growth hormone
PT	secretagogue receptor, or treating a metabolic disorder.
XX	
PS	Disclosure; Page 94-95; 100pp; English.
XX	
CC	The present invention relates to the use of a zsig33 peptide for forming
CC	a peptide-antibody complex, purifying a peptide, inhibiting signal
CC	transduction in a cell expressing a growth hormone secretagogue receptor
CC	(GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
CC	of a mammal, inhibiting growth hormone secretion in pituitary cells of a
CC	mammal, or treating a metabolic disorder. The peptide is useful for
CC	forming a peptide-antibody complex, purifying a peptide, inhibiting
CC	signal transduction in a cell expressing a GHS-R, decreasing fat
CC	deposition in a mammal, suppressing the appetite of a mammal, inhibiting
CC	growth hormone secretion in pituitary cells of a mammal, or treating a
CC	metabolic disorder. The zsig33 polypeptides can be used to study
CC	proliferation or differentiation in stomach, lung, pituitary,
CC	hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
CC	skeletal muscle or pancreas. They are also useful in delivering
CC	therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
CC	also useful for promoting wound healing. The polypeptides, nucleic acids
CC	and antibodies are useful for diagnosing, treating or preventing
CC	disorders associated with gastric reflux, gastroparesis, modulation of
CC	secretion of pituitary hormones, including growth hormone, Crohn's
CC	disease, metabolic wasting, gastric ulcers, weight management, or
CC	degenerative disease. The present sequence is the human motilin receptor
CC	GPR38A coding sequence shown in the exemplification of the invention.
XX	
SQ	Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;
Query Match	100.0%; Score 1239; DB 12; Length 1239;
Best Local Similarity	100.0%; Pred. No. 3e-215;
Matches 1239; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGGACAGCCCTGGAAACGGACGACGCGCCCGAGGGGGCGCGGAGCCCGCGTGGCCCC 60
	1 ATGGGACAGCCCTGGAAACGGACGACGCGCCCGAGGGGGCGCGGAGCCCGCGTGGCCCC 60
61	CGCTGCGCGCTTGGACGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGGCGCTGGTGGCG 120
61	CGCTGCGCGCTTGGACGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGGCGCTGGTGGCG 120
121	GTGACCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
121	GTGACCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
181	ATGCTGATCGGGCGCTACCGGACATGCGGACCAACCACTTGTACTTGGGAGCATG 240
181	ATGCTGATCGGGCGCTACCGGACATGCGGACCAACCACTTGTACTTGGGAGCATG 240
241	GCCGTGTCGACCTACTCTGCTCGGGCTGCGCTTGCAGCTTACCGCTCTGGGCGC 300
241	GCCGTGTCGACCTACTCTGCTCGGGCTGCGCTTGCAGCTTACCGCTCTGGGCGC 300
301	TGCGGGCGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
301	TGCGGGCGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
361	TGCACCTACGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361	TGCACCTACGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421	TGCGCGCGCTTCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421	TGCGCGCGCTTCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481	GTGCTGCTGGGCGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481	GTGCTGCTGGGCGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
541	CAGAACCCCGCGCATCTCGTAGTCCCGGCTCAATGSCACCGCGGATGCGCTCTCTCG 600
541	CAGAACCCCGCGCATCTCGTAGTCCCGGCTCAATGSCACCGCGGATGCGCTCTCTCG 600
601	CCTCTCGGCTGCTGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
601	CCTCTCGGCTGCTGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
661	GGGCGCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
661	GGGCGCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
721	CAGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721	CAGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781	CTGTGCTTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGGAGCAGCGCGGCGCG 840
781	CTGTGCTTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGGAGCAGCGCGGCGCGCG 840
841	CTGCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
841	CTGCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
901	CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
901	CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
961	TACATAACACGGAAGATTTCGCGGATGATGCTTCTCTCAGTACTTTAAACATCTCGCT 1020
961	TACATAACACGGAAGATTTCGCGGATGATGCTTCTCTCAGTACTTTAAACATCTCGCT 1020
1021	CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080
1021	CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080
1081	AAGTACAGAGCGCGCGCTTTAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140



Db 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTCTCGAAGGAAGTCCAGGCGGAGAGGCTTC 1140  
 Qy 1141 CACAGAAGCAGGACACTCGCGGGGAGTTCAGGGGACACTGGAGGACACGCTGGGC 1200  
 Db 1141 CACAGAAGCAGGACACTCGCGGGGAGTTCAGGGGACACTGGAGGACACGCTGGGC 1200  
 Qy 1201 TACACCGAGACAAGCGCTTAACGTGAAGACGATGGGATAA 1239  
 Db 1201 TACACCGAGACAAGCGCTTAACGTGAAGACGATGGGATAA 1239

## RESULT 7

AD030072  
 ID AD030072 standard; cDNA; 1239 BP.

XX AD030072;

AC AD030072;

DT 29-JUL-2004 (first entry)

XX Human GPCR GPR38 polynucleotide, SEQ ID NO:1174.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 KW cytotatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KW gene; ss.

XX Homo sapiens.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409103P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;

XX WPI; 2004-390329/36.

DR P-PSDB; ADO29697.

XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 1174; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising

CC probes which hybridise to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 CC nucleic acid of the invention. Note: The full sequence data for this  
 CC patent did not form part of the printed specification; those sequences  
 CC not shown were obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

	Query Match	Best Local Similarity	Score 1239;	DB 12;	Length 1239;
Qy	1	100.0%;	100.0%;	0;	0;
Db	1	100.0%;	100.0%;	0;	0;
Qy	61	100.0%;	100.0%;	0;	0;
Db	61	100.0%;	100.0%;	0;	0;
Qy	121	100.0%;	100.0%;	0;	0;
Db	121	100.0%;	100.0%;	0;	0;
Qy	181	100.0%;	100.0%;	0;	0;
Db	181	100.0%;	100.0%;	0;	0;
Qy	241	100.0%;	100.0%;	0;	0;
Db	241	100.0%;	100.0%;	0;	0;
Qy	301	100.0%;	100.0%;	0;	0;
Db	301	100.0%;	100.0%;	0;	0;
Qy	361	100.0%;	100.0%;	0;	0;
Db	361	100.0%;	100.0%;	0;	0;
Qy	421	100.0%;	100.0%;	0;	0;
Db	421	100.0%;	100.0%;	0;	0;
Qy	481	100.0%;	100.0%;	0;	0;
Db	481	100.0%;	100.0%;	0;	0;
Qy	541	100.0%;	100.0%;	0;	0;
Db	541	100.0%;	100.0%;	0;	0;
Qy	601	100.0%;	100.0%;	0;	0;
Db	601	100.0%;	100.0%;	0;	0;
Qy	661	100.0%;	100.0%;	0;	0;



Db 661 GGGCCGAGACCGCGGCGCGCTGTTACCGCGAATCGCGCGAGCCCGCG 720  
Qy 721 CAGCTGGGCGCGCTCGGTGTATGCTGTGGGTACACCGCGCTACTTCTTCTGCGCTTT 780  
Db 721 CAGCTGGGCGCGCTCGGTGTATGCTGTGGGTACACCGCGCTACTTCTTCTGCGCTTT 780  
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGTGTGAGCAGCGCGGCGG 840  
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGTGTGAGCAGCGCGGCGG 840  
Qy 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGGAGCGCCGCGACCGTTCGGGTCTG 900  
Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGGAGCGCCGCGACCGTTCGGGTCTG 900  
Qy 901 CTGTGTGGTGTCTGGCATTTTATAATTTGCTGTGGTTCCTTCCAGCTTGGCAGATCAT 960  
Db 901 CTGTGTGGTGTCTGGCATTTTATAATTTGCTGTGGTTCCTTCCAGCTTGGCAGATCAT 960  
Qy 961 TACATAAACACGGAAGATTCGGGATGATGATCTCTCAGTACTTTAAACATCGTCT 1020  
Db 961 TACATAAACACGGAAGATTCGGGATGATGATCTCTCAGTACTTTAAACATCGTCT 1020  
Qy 1021 CTGCAACTTTCTATCTGAGCGCATCTATCAACCAATCCTCTACAACTCATTTCAA 1080  
Db 1021 CTGCAACTTTCTATCTGAGCGCATCTATCAACCAATCCTCTACAACTCATTTCAA 1080  
Qy 1081 AAGTACAGACGGCGCGCTTTAAATCTGCTGCTGCAAGGAGTCCAGCGCGAGGCTTC 1140  
Db 1081 AAGTACAGACGGCGCGCTTTAAATCTGCTGCTGCAAGGAGTCCAGCGCGAGGCTTC 1140  
Qy 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGCGAGGACACTTGGAGGAGACACGTTGGC 1200  
Db 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGCGAGGACACTTGGAGGAGACACGTTGGC 1200  
Qy 1201 TACACCGAGACAGCGCTTAACGTGAAGACGATGGGATAA 1239  
Db 1201 TACACCGAGACAGCGCTTAACGTGAAGACGATGGGATAA 1239  
RESULT 8  
ADQ37920  
ID ADQ37920 standard; DNA; 1239 BP.  
XX  
AC ADQ37920;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human G-protein-coupled receptor 38 coding sequence.  
XX  
KW ds; gene; antiparkinsonian; neuroprotective; nootropic; cardiovascular;  
KW cardiac; vasotropic; antiarteriosclerotic; nephrotropic; utroptic;  
KW urology disease; cardiovascular disease;  
KW peripheral nervous system disorder; central nervous system disorder;  
KW G-protein-coupled receptor 38; GPR38; Parkinson's disease;  
KW multiple sclerosis; dementia; myocardial infarction; ischemic disease;  
KW atherosclerosis; renal failure; glomerulopathy; urinary incontinence.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1239  
FT /\*tag= a  
FT /product= "G-coupled receptor protein 38"  
XX  
FN WO2004057328-A2.  
XX  
PD 08-JUL-2004.  
XX  
PF 11-DEC-2003; 2003WO-EP014052.  
XX  
PR 23-DEC-2002; 2002EP-00028753.  
XX

(FARB ) BAYER HEALTHCARE AG.  
Golz S, Brueggemeier U, Summer H;  
WPI; 2004-543310/52.  
P-PSDB; ADQ37921.  
Screening therapeutic agents for use in treatment of urology diseases and cardiovascular diseases in a mammal, comprises contacting a test compound with G-protein-coupled receptor 38, and detecting binding.  
Disclosure; SEQ ID NO 1; 111pp; English.  
The invention relates to a method of screening (M1) for therapeutic agents useful in the treatment of a disease chosen from urology diseases, cardiovascular diseases and disorders of the peripheral and central nervous system in a mammal, comprises contacting a test compound with a G-protein-coupled receptor 38 (GPR38) polypeptide, and detecting binding of the test compound to the GPR38 polypeptide. (M1) is useful for screening therapeutic agents useful in the treatment of a disease chosen from urology diseases, cardiovascular diseases and disorders of the peripheral and central nervous system in a mammal, such as Parkinson's disease, multiple sclerosis, dementia, cardiovascular disorders such as myocardial infarction, ischemic diseases, atherosclerosis, and urological disorders such as acute or chronic renal failure, glomerulopathies, and urinary incontinence. This sequence corresponds to the nucleic acid encoding the human G-protein-coupled receptor 38.  
Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1239; DB 12; Length 1239;  
Best Local Similarity 100.0%; Pred. No. 3e-215;  
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGGCGAGCCCTCGAAGCGGAGCGCGCCCGGCGGCGCGCGCGCGCGCGCG 60  
Db 1 ATGGGCGAGCCCTCGAAGCGGAGCGCGCCCGGCGGCGCGCGCGCGCGCGCG 60  
Qy 61 GCGCTGCGCGCTTGGAGCGCGCGCTGCTGCGCCCTTTCCCGTGGGCGCGTGGTGG 120  
Db 61 GCGCTGCGCGCTTGGAGCGCGCGCTGCTGCGCCCTTTCCCGTGGGCGCGTGGTGG 120  
Qy 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCGGGGTGAGCGGCAACGTCGTCG 180  
Db 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCGGGGTGAGCGGCAACGTCGTCG 180  
Qy 181 ATGCTGATCGGGCGCTACCGGAGCATCGGACACCAACCACTTGTACTCGGAGCATG 240  
Db 181 ATGCTGATCGGGCGCTACCGGAGCATCGGAGACCAACCACTTGTACTCGGAGCATG 240  
Qy 241 GCCGTGTCGACCTACTCATCTGCTCGGGGTGCGCTTTCGACCTGTACCGCTCTGGCG 300  
Db 241 GCCGTGTCGACCTACTCATCTGCTCGGGGTGCGCTTTCGACCTGTACCGCTCTGGCG 300  
Qy 301 TCGCGGCGCTGGGTGTGCGGCGCGCTGTGCGCGCTGTCCCTTACGTGGGCGAGGCG 360  
Db 301 TCGCGGCGCTGGGTGTGCGGCGCGCTGTGCGCGCTGTCCCTTACGTGGGCGAGGCG 360  
Qy 361 TGCACCTACCGCAGCTGTGCATGACCGCGCTGACCGCTGTACTGCGCATC 420  
Db 361 TGCACCTACCGCAGCTGTGCATGACCGCGCTGACCGCTGTACTGCGCATC 420  
Qy 421 TCGCGCGCGCTTCGCGCGCGCGCTTGTGTACACCGCGCGCGCTCGCGCGCTCATCGCT 480  
Db 421 TCGCGCGCGCTTCGCGCGCGCGCTTGTGTACACCGCGCGCGCTCGCGCGCTCATCGCT 480  
Qy 481 GTGCTCTGGGCGGTGGGCGTCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 481 GTGCTCTGGGCGGTGGGCGTCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Qy 541 CAGGACCGCGCATCTCGGTAGTCCCGGCGCTCAATGGCACCGCGCGATCGCTCTCTCG 600  
Db 541 CAGGACCGCGCATCTCGGTAGTCCCGGCGCTCAATGGCACCGCGCGATCGCTCTCTCG 600



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Db 808 CAGGACCCCGGATCTCCGTAGTCCCGGCCCTCAATGGACCGCGGATCGCCCTCCCTCG 867
Qy 601 CCTCTCGCCTCGTCCGCGCTCTCTGGCTCTCGCGGGGCCACACCGCCGCTCCCGCGCTCG 660
Db 868 CCTCTCGCCTCGTCCGCGCTCTCTGGCTCTCGCGGGGCCACACCGCGCTCCCGCGCTCG 927
Qy 661 GGGCCCGAGACCGCGGAGCCGCGCGCTGTTACGCGCGGAATGCGCGCGAGCCCGCGG 720
Db 928 GGGCCCGAGACCGCGGAGCCGCGCGCTGTTACGCGCGGAATGCGCGCGAGCCCGCGG 987
Qy 721 CAGCTGGGCGCTCGCTGTCTATCTGTGGTTCACACCGCTACTCTTCTCTGCGCTTT 780
Db 988 CAGCTGGGCGCTCGCTGTCTATCTGTGGTTCACACCGCTACTCTTCTCTGCGCTTT 1047
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCGCG 840
Db 1048 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCGCG 1107
Qy 841 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTTCGCGTCTCG 900
Db 1108 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTTCGCGTCTCG 1167
Qy 901 CTGCTGGTGTCTCGCATTTATATTGCTGTTGCCCTTCCAGTTGGCAGATCATT 960
Db 1168 CTGCTGGTGTCTCGCATTTATATTGCTGTTGCCCTTCCAGTTGGCAGATCATT 1227
Qy 961 TACATAAACACGGAAGATTGCGGGATGATGACTTCTCTCAGTACTTTAAACATCTCGCT 1020
Db 1228 TACATAAACACGGAAGATTGCGGGATGATGACTTCTCTCAGTACTTTAAACATCTCGCT 1287
Qy 1021 CTGCAACTTTTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCAATTTCAAAG 1080
Db 1288 CTGCAACTTTTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCAATTTCAAAG 1347
Qy 1081 AGTTACAGCGCGCGCTTTAACTGCTGCTCGCAAGGAGTCCAGCGCGAGGCTTC 1140
Db 1348 AGTTACAGCGCGCGCTTTAACTGCTGCTCGCAAGGAGTCCAGCGCGAGGCTTC 1407
Qy 1141 CACAGAAGCAGGACACTCGCGGGGAAGTTGAGGGGACACTGAGGAGACACAGTGGCG 1200
Db 1408 CACAGAAGCAGGACACTCGCGGGGAAGTTGAGGGGACACTGAGGAGACACAGTGGCG 1467
Qy 1201 TACACCGAGACAGCGCTAACTGAAGACGATGGGATAA 1239
Db 1468 TACACCGAGACAGCGCTAACTGAAGACGATGGGATAA 1506

```

## RESULT 10

AAZ45404

ID AAZ45404 standard; cdna; 1390 BP.

XX AC AAZ45404;

XX XX

XX 27-MAR-2000 (first entry)

XX DE

XX cDNA encoding the motilin receptor splice variant MTL-R1B.

XX KW Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;

XX KW spliced form; MTL-R1A; MTL-R1B; Gastric motility disorder;

XX KW functional defect; neurological disorder; scleroderma; colonoscopy;

XX KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;

XX KW infection; stress-related motility disorder; psychogenic disorder;

XX KW gastroparesis; gastro-oesophageal reflux disease; constipation;

XX KW chronic idiopathic pseudo obstruction; acute faecal impaction;

XX KW postoperative ileus; gallstones; infantile colic; diarrhoea;

XX KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;

XX KW endoscopy; duodenal intubation; ds.

XX OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

XX FH 1. .1161

XX CDS

XX FT

XX

XX

XX

XX

XX

XX

FT FT /\*tag= a  
 XX XX /product= "MTL-R1B"

PN WO9964436-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012773.

XX 12-JUN-1998; 98US-0089098P.

XX (MERI ) MERCK & CO INC.

XX Feighner SD, Patchett AA, Tan C, Mckee K, Macneil D, Howard AD;

XX Pong S, Smith RG;

XX WPI; 2000-105868/09.

XX P-PSDB; AAY54146.

XX Novel receptor protein for screening compounds used in treating irritable

XX bowel syndrome, constipation and other gastric conditions.

XX Claim 6; Fig 4; 44pp; English.

XX The present sequence encodes splice variant MTL-R1B of the motilin

XX receptor. The gene encodes a G-protein coupled receptor, and is

XX designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A

XX (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven

XX transmembrane domain form, and MTL-R1B is a truncated five transmembrane

XX domain. The MTL-R1 proteins are used to identify agonists and antagonists

XX which can be used for treating gastric motility disorders, functional

XX defects, disorders secondary to neurological disorders e.g. scleroderma,

XX paraneoplastic syndromes radiation induced dysmotility, diabetes,

XX infections, stress-related motility disorders, psychogenic disorders,

XX gastroparesis, gastro-oesophageal reflux disease, constipation, chronic

XX idiopathic pseudo obstruction, acute faecal impaction, postoperative

XX ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer

XX dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used

XX in the preparation for colonoscopy, endoscopy and duodenal intubation

XX SQ Sequence 1390 BP; 190 A; 496 C; 436 G; 268 T; 0 U; 0 Other;

XX

XX Query Match 87.0%; Score 1078; DB 3; Length 1390;

XX Best Local Similarity 89.1%; Pred. No. 4.3e-186;

XX Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

Qy 1 ATGGGCGAGCCCTCGAACGGCAGCAGCGGCCCGGAGGGGGCGGAGCGCCGCTGGGCGCC 60

Db 1 ATGGGCGAGCCCTCGAACGGCAGCAGCGGCCCGGAGGGGGCGGAGCGCCGCTGGGCGCC 60

Qy 61 GCGCTGCGCGCTTGGCAGCGCGCGCTGCTCGCCCTTTTCCCTGGGGGCGCTGTGCGCG 120

Db 61 GCGCTGCGCGCTTGGCAGCGCGCGCTGCTCGCCCTTTTCCCTGGGGGCGCTGTGCGCG 120

Qy 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

Db 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

Qy 181 ATGCTGTATCGGGCGCTACCGGGACATCGGACACACCAACCACTTGTACTCGGGCAGCATG 240

Db 181 ATGCTGTATCGGGCGCTACCGGGACATCGGACACACCAACCACTTGTACTCGGGCAGCATG 240

Qy 241 GCGGTGTCCGACCTACTCATCTGTCTGGGCTGCGCTTTCGACCTGTACCGCTCTGTGGCG 300

Db 241 GCGGTGTCCGACCTACTCATCTGTCTGGGCTGCGCTTTCGACCTGTACCGCTCTGTGGCG 300

Qy 301 TCGGGCGCCTGGGTGTGCGGCGCGCTGCTGTGCGCGCTGTGCTGTGCTGTGCTGTGCTGTG 360

Db 301 TCGGGCGCCTGGGTGTGCGGCGCGCTGCTGTGCGCGCTGTGCTGTGCTGTGCTGTGCTGTG 360

Qy 361 TGCACCTACGCCACGCTGCTGCATACATACCGCGCTCAGCGTTCGAGCGGTACTCGGCCATC 420

Db 361 TGCACCTACGCCACGCTGCTGCATACATACCGCGCTCAGCGTTCGAGCGGTACTCGGCCATC 420

QY 421 TCGCGCGCTCCGCGCGCGCTTGTGTACCCGCGCGCGCTCGCGCGCTCATCGCT 480  
 Db 421 TCGCGCGCTCCGCGCGCGCTTGTGTACCCGCGCGCGCTCGCGCGCTCATCGCT 480  
 QY 481 GTGCTCTGGCGCGTGGCGTCTCTCTCGCGTCCCTTCTTCTTCTGGTGGCGTCGAG 540  
 Db 481 GTGCTCTGGCGCGTGGCGTCTCTCTCGCGTCCCTTCTTCTTCTGGTGGCGTCGAG 540  
 QY 541 CAGGACCCCGGATCTCGGTAGTCTCGCGGCTCAATGGACCGCGCGGATCGCTCTCTCG 600  
 Db 541 CAGGACCCCGGATCTCGGTAGTCTCGCGGCTCAATGGACCGCGCGGATCGCTCTCTCG 600  
 QY 601 CCTCTCGCTCTCGCGCGCTCTCTCTCGCGGCGCGACCGCGCTCCCGCGCTCG 660  
 Db 601 CCTCTCGCTCTCGCGCGCTCTCTCTCGCGGCGCGACCGCGCTCCCGCGCTCG 660  
 QY 661 GGGCCCGAGACCGCGGCGCGCGCTGTTCAGCGCGAATGCGCGCGAGCCCGCG 720  
 Db 661 GGGCCCGAGACCGCGGCGCGCGCTGTTCAGCGCGAATGCGCGCGAGCCCGCG 720  
 QY 721 CAGCTGGCGCGCTCGGTGTCTATGTGTGGGTCAACCGCGCTACTTCTTCTGCGCTTT 780  
 Db 721 CAGCTGGCGCGCTCGGTGTCTATGTGTGGGTCAACCGCGCTACTTCTTCTGCGCTTT 780  
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 Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGTCAACCGCGCTACTTCTTCTGCGCTTT 840  
 QY 841 CTGCGAGGCGCGCGCTCTCGGGGCGGAGAGAGCGCGCGAGAGCGCTCGCGCTCTG 900  
 Db 841 CTGCGAGGCGCGCGCTCTCGGGGCGGAGAGAGCGCGCGAGAGCGCTCGCGCTCTG 900  
 QY 901 C----- 901  
 Db 901 CGTAAGTGGAGCGCGGTGTTCCAAAGACGCTGCTGCGCGCGCGCGGAGC 960  
 QY 902 ----- 901  
 Db 961 GCGCAACGCTGGTGTCCCTCTCGCGCGAGCTCTGGGCGCGCTTCAGCTCCC 1020  
 QY 902 -----TGTTGGTGGTCTTGGCATTTATTAATTG 929  
 Db 1021 TTTCTTATTTGATTCCAGCTCCACCGCGCGTGTGGTCTTGGCATTTATTAATTG 1080  
 QY 930 CTGGTTGCCCTTCCAGTTGGCAGATCATTTACATAACAGGAGATTCGCGATGAT 989  
 Db 1081 CTGGTTGCCCTTCCAGTTGGCAGATCATTTACATAACAGGAGATTCGCGATGAT 1140  
 QY 990 GTACTTCTCTAGTACTTTAACTGCTGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1049  
 Db 1141 GTACTTCTCTAGTACTTTAACTGCTGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1200  
 QY 1050 CAACCAATCTCTCAACCTCATTTCAAAGAGTACAGAGCGCGCGCTTTAAACTGCT 1109  
 Db 1201 CAACCAATCTCTCAACCTCATTTCAAAGAGTACAGAGCGCGCGCTTTAAACTGCT 1260  
 QY 1110 GTCTGCAAGGAGTCTCAGCGCGAGAGGCTTCCACAGAGAGGAGACACTGGGGGGAAGT 1169  
 Db 1261 GCTCGCAAGGAGTCTCAGCGCGAGAGGCTTCCACAGAGAGGAGACACTGGGGGGAAGT 1320  
 QY 1170 TGCAGGGGACACTGGAGGAGACACGGTGGGCTTACACCGAGACAAGCGCTAAGTCAAGAC 1229  
 Db 1321 TGCAGGGGACACTGGAGGAGACACGGTGGGCTTACACCGAGACAAGCGCTAAGTCAAGAC 1380  
 QY 1230 GATGGGATAA 1239  
 Db 1381 GATGGGATAA 1390

RESULT 11  
 AAF85448  
 ID AAF85448 standard; cdna; 1203 BP.

XX AAF85448;  
 AC 23-JUL-2001 (first entry)  
 XX Nucleotide sequence of a rabbit motilin receptor polypeptide.  
 DE Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW gastroparesis; irritable bowel syndrome; diarrhoea; ss.  
 XX Oryctolagus cuniculus.  
 PH Key Location/Qualifiers  
 CDS 1..1203  
 FT /\*tag= a  
 FT /note= "motilin receptor"  
 XX WO200132710-A1.  
 XX 10-MAY-2001.  
 XX 25-OCT-2000; 2000MO-US029426.  
 XX 29-OCT-1999; 99US-0162264P.  
 XX (MERI ) MERCK & CO INC.  
 XX Tan C, McKee K;  
 XX WPI; 2001-343479/36.  
 XX P-PSDB; AAB68477.  
 XX Novel polypeptides related to dog and rabbit motilin receptor  
 PT polypeptide, comprising unique regions from dog and motilin receptor  
 PT amino acid sequence, useful for identifying compounds for treating  
 PT diarrhea in humans.  
 XX Claim 18; Page 18-19; 42pp; English.  
 CC The present sequence encodes a rabbit motilin receptor polypeptide. The  
 CC specification describes an unique sequence present in exon 1 of the dog  
 CC motilin receptor, which is not present in human or Sphaeroides nephelus  
 CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is  
 CC useful for measuring the ability of a compound to affect motilin receptor  
 CC activity. Motilin receptor polynucleotides and polypeptides are used to  
 CC identify therapeutic compounds which are useful for treating  
 CC gastrointestinal diseases and disorders such as gastric motility  
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea  
 XX SQ Sequence 1203 BP; 154 A; 423 C; 403 G; 223 T; 0 U; 0 Other;  
 Query Match 73.9%; Score 915.6; DB 4; Length 1203;  
 Best Local Similarity 85.5%; Pred. No. 1.1e-156;  
 Matches 1058; Conservative 0; Mismatches 144; Indels 36; Gaps 2;  
 QY 1 ATGGGCGAGCCCTCGAACGGCAGCGAGCGGCGCGGCGCGGAGCGCGCGCGCGCC 60  
 Db 1 ATGGGCGAGCCCTCGAACGGCAGCGAGCGGCGCGGCGCGGAGCGCGCGCGCGCGCC 60  
 QY 61 CGCGTCCGCGCTTGGCAGCGAGCGCGCTGTCTGCGCTTTTCCCTTGGGGCGCTGTGTGCG 120  
 Db 61 CGCGTCCGCGCTTGGCAGCGAGCGCGCTGTCTGCGCTTTTCCCTTGGGGCGCTGTGTGCG 120  
 QY 121 GTGACCGCTGTGTGCTGTGCTGTCTGCTCGGGGTGAGCGGCAAGCTGTGACCGGTG 180  
 Db 121 GTGACCGCGCTGTGTGCTGTGCTGTCTGCGGCTGTCTGCGGCTGTGAGCGCAACCTGTG 180  
 QY 181 ATGCTGTATCGGGCGCTACCGGGACATGCGGACACACCACTTGTACTTGGGAGCATG 240  
 Db 181 CTGCTGTATCGGGCGCTACCGGGACATGCGGACACCACTTGTACTTGGGAGCATG 240  
 QY 241 CGCGTGTCCGACCTACTCATCTCTGCTGGGTGCGGTTCGACCTGTACCGCTCTGGGCGC 300

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Db 241 GCCGTGTCGACCTGCTCATCTCTGCTGGGCTGCCCTTCGACCTGTACCGCCTGTGGGCG 300
Qy 301 TCGCGCCCTGGGTGTTGGGCGCGTGTCTTCGCCGCTGTCCCTCTACGTGGCGAGGGC 360
Db 301 TCGAGGCCCTGGGTGTTGGGACAGCTGCTCTCGCGCCTGTCTGTACGTGGCGAGGGC 360
Qy 361 TCGACCTAGCCACGCTGTGTACATGACCGGCTCAGGTCGAGGCTACCTTGGCCATC 420
Db 361 TCGACCTAGCCCTGCTGTGTACATGACCGGCTCAGGTCGAGGCTACCTTGGCCATC 420
Qy 421 TCGCGCCGCTCGCGCGCGCTGTTGTCACCGCGCGCTCGCGCGCTCATCGCT 480
Db 421 TCGCGCCGCTCGCGCGCGCTGTTGTCACCGCGCGCTCGCGCGCTCATCGCC 480
Qy 481 GTGCTCTGGGCGCGTGTCTCTGCGGCTCCCTTCTTCTTCTGTGGGCTCGAG 540
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Qy 541 CAGGACCCCGGATCTCGGTAGTTCGGGCGCTCAATGGCACCGCGGATCGCTCTCG 600
Db 541 CAGGACCCCGGCTCTTCGGGCGCGGACCGACCGGTACTGTGCGGTGGACCCCTCG 600
Qy 601 CCTCTCGCTCTGCGCGCTCTCTGCGCTCTGCGGCGCACCGCGTCCCGCGCTCG 660
Db 601 TCGCCGCGC-----CCGCGCTCCCGCGCTCG 627
Qy 661 GGGCCCGAGACCGCGAGCGCGGCTGTTTCAGCGCGAATGCGCGGAGCCCGCG 720
Db 628 GGGCCCG--GAGCGAGCGCGGCTCTGTTACGCGCGAGTGCAGCGCGCGCG 684
Qy 721 CAGCTGGGCGCGCTGCTGTATGCTGTGGGTACACCGCTACTTCTTCTTCTGCTT 780
Db 685 CAGCTGGGCTGCTGCGGCTATGCTGTGGGTACACCGCTACTTCTTCTTCTGCTT 744
Qy 781 CTGTCCTCAGCATCTCTACCGGCTCATCGGCGGAGCTGTGAGCAGCGCGGCG 840
Db 745 CTCTGCTCAGCATCTCTACCGGCTCATCGGCGGAGCTGTGCGGCGCG 804
Qy 841 CTGCGAGGCGCGCGCTCGGGGCGGAGAGGCGCACCGCGAGCGTTCGCGTCTCTG 900
Db 805 CTGCGAGGCGCGCGCGCGCGCGGTCGGGAGAGGCGCACCGCGAGCGTTCGCTCTG 864
Qy 901 CTGCTGGTGTCTGGCATTTAATTTGCTGGTGGCTTCCAGTTGGGAGAAATCAAT 960
Db 865 CTGCTGGTGTCTGGCTTTATAGTGTGCTGGCTTCCAGTTGGGAGGATCAAT 924
Qy 961 TACATAAACACGAGATTCGCGGATGATGTTCTCTCAGTACTTTTAAATCTGCT 1020
Db 925 TACATAAACACCAAGACTCGCGGATGATGTTCTCTCCAGTACTTTTAAATCTGCTG 984
Qy 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTACAACCTCATTTCAA 1080
Db 985 CTGCGAGTTTCTACTGAGTGGTCTCATCAACCAATCTCTACAACCTCATTTCAA 1044
Qy 1081 AAGTACAGAGCGCGCTTTAAATCTGTGTCGAAGAACTTCAGGCGGAGAGGCTTC 1140
Db 1045 AAGTACAGAGCGGCTGCGCGAGACTGTCTGCGGAAAGCCGAGCGGCGCCAGTGTG 1104
Qy 1141 CACAGACGAGGACACTCGGGGAGTTGCGAGGAGACACTGGAGGAGACAGTGGGC 1200
Db 1105 TCGGAAAGCAGGGGCGCTGAGCAGACGTTGAGGAGGACACTGGCGGAGACAGCTGG 1164
Qy 1201 TACACCGAGACAGCGCTAACTGAAGACGATGGGATA 1238
Db 1165 TCGACCGAGACCGGCTTAACAAAGACGGCTGGATA 1202
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RESULT 12

AAF83684

ID AAF83684 standard; DNA; 1161 BP.

XX

AC AAF83684;

XX

DT 23-JUL-2001 (first entry)

XX Short form of motilin receptor, GPR-38B isoform encoding DNA.

XX zsig33; signal transduction; hormone; enzyme; neural development;  
XX gastric contractility; nutrient uptake; digestive; pancreatic; human;  
XX insulin-like growth factor-I; growth hormone; bone; gastrointestinal;  
XX glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R; ds;  
XX G-protein coupled receptor; motilin receptor; GPR38; GPR-38B; isoform.

OS Homo sapiens.

XX Key Location/Qualifiers

FH CDS 1..1161

FT /\*tag= a

FT /product= "GPR-38B"

XX WO200138355-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032074.

XX 22-NOV-1999; 99US-0166765P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI; 2001-355879/37.

XX P-PSDB; AAB62653.

XX Forming reversible peptide receptor complex for purifying cell and  
XX peptides, stimulating signal transduction and modulating hormone  
XX secretion, involves contacting a receptor with zsig33 polypeptide.

XX Disclosure; Page 106-109; 11pp; English.

XX The invention relates to a method of forming a reversible peptide-  
XX receptor complex that involves providing an immobilized receptor, and  
XX contacting the receptor with a zsig33 peptide (comprising residues 24-37  
XX of AAB62649), where the receptor binds to the zsig33 peptide. The method  
XX is useful for purifying cells, purifying a peptide, stimulating signal  
XX transduction in a cell expressing a receptor. It is also useful for  
XX modulating secretion of hormones, neural development and/or utilization,  
XX gastric contractility, nutrient uptake, secretion of digestive and  
XX pancreatic enzymes and hormones, secretion of insulin-like growth factor  
XX -I, secretion of non-zsig33 proteins. It is useful for modulating growth  
XX hormone secretion in a mammal having a disease associated with abnormal  
XX levels of growth hormone, such as osteoporosis, bone repair, bone  
XX remodeling, low osteoblast levels, cartilage repair and remodeling,  
XX skeletal dysplasia, immune suppression, obesity, growth retardation,  
XX protein catabolic responses after surgery, cachexia, protein loss,  
XX dwarfism, wound healing and ovulation induction, treating a mammal having  
XX a metabolic disorder requiring neurological feedback, such as satiety  
XX regulation, glucose absorption and metabolism and neuropathy-associated  
XX gastrointestinal disorders, and stimulating glucose-induced insulin  
XX release in a mammal. The present sequence represents the DNA encoding the  
XX short form of motilin receptor, GPR-38B (one of the two isoforms of GPR38  
XX which result from alternative splicing). GPR38 has homology to the human  
XX G-protein coupled receptor, GHS-R

SQ Sequence 1161 BP; 126 A; 436 C; 372 G; 227 T; 0 U; 0 Other;

.. Query Match 72.7%; Score 901; DB 4; Length 1161;

.. Best Local Similarity 100.0%; Pred. No. 4.9e-154;

Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGGACGCCCCCTGGACGCGAGCGGCCCCCGAGGGGGCGGAGCCCGCTGGGCC 60

Qy 61 CGCTGCGCGCTTGGACGAGCGCGCTGTCTGCCCTTTTCCCTTGGGGGCGCTGTGCGG 120















GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:55 ; Search time 203.635 Seconds  
(without alignments)  
9955.765 Million cell updates/sec

Title: US-09-719-485-2  
Perfect score: 1239  
Sequence: 1 atgggcgcgcctggaaagg.....acgtgaagacatgggataa 1239

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	22.8	283	US-08-993-088A-4	Sequence 4, Appli
2	283	22.8	283	US-08-993-424B-4	Sequence 4, Appli
3	283	22.8	283	US-09-603-680-4	Sequence 4, Appli
4	255.8	20.6	1050	US-09-762-661A-1	Sequence 1, Appli
5	234.8	19.0	1063	US-09-077-675A-1	Sequence 1, Appli
6	234.8	19.0	1063	US-09-077-675A-1	Sequence 1, Appli
7	231.6	18.7	1095	US-09-743-475-2	Sequence 2, Appli
8	231.6	18.7	4009	US-09-743-475-1	Sequence 1, Appli
9	230	18.6	1029	US-09-077-675A-4	Sequence 4, Appli
10	230	18.6	1029	US-09-077-674-4	Sequence 4, Appli
11	229.8	18.5	1092	US-09-077-675A-15	Sequence 15, Appl
12	229.8	18.5	1092	US-09-077-674-15	Sequence 15, Appl
13	229	18.5	250	US-09-016-434-359	Sequence 359, App
14	228.8	18.5	1122	US-09-077-675A-9	Sequence 9, Appli
15	228.8	18.5	1122	US-09-077-674-9	Sequence 9, Appli
16	228.4	18.4	3129	US-09-077-675A-14	Sequence 14, Appl
17	228.4	18.4	3129	US-09-077-674-14	Sequence 14, Appl
18	227.8	18.4	1088	US-09-077-675A-6	Sequence 6, Appli
19	227.8	18.4	1088	US-09-077-674-6	Sequence 6, Appli
20	227.8	18.4	1101	US-09-016-434-1148	Sequence 1148, Ap
21	227.8	18.4	1101	US-09-170-496D-87	Sequence 87, Appl
22	227.8	18.4	1101	US-09-170-496D-209	Sequence 209, App
23	227.8	18.4	1101	US-09-364-425B-44	Sequence 44, Appl
24	153	12.3	836	US-09-077-675A-11	Sequence 11, Appl
25	153	12.3	836	US-09-077-674-11	Sequence 11, Appl
26	134.8	10.9	729	US-09-684-725-1	Sequence 1, Appli
27	134.8	10.9	1239	US-09-949-016-4230	Sequence 4230, Ap

28	134.8	10.9	1248	3	US-09-545-944-1	Sequence 1, Appli
29	134.8	10.9	1360	4	US-09-341-016A-2	Sequence 2, Appli
30	134.8	10.9	16914	4	US-09-949-016-15972	Sequence 15972, A
31	132	10.7	1575	3	US-08-858-876A-1	Sequence 1, Appli
32	132	10.7	1575	3	US-09-472-880-1	Sequence 1, Appli
33	127.2	10.3	1233	4	US-08-826-509-536	Sequence 536, App
34	125.4	10.1	1342	3	US-08-832-339-1	Sequence 1, Appli
35	125.4	10.1	1342	3	US-08-832-339-1	Sequence 1, Appli
36	123	9.9	1257	4	US-09-826-509-534	Sequence 534, App
37	123	9.9	4080	4	US-09-016-434-1346	Sequence 1346, Ap
38	122.8	9.9	1529	3	US-08-858-876A-3	Sequence 3, Appli
39	122.8	9.9	1529	3	US-09-472-880-3	Sequence 3, Appli
40	122	9.8	1095	4	US-08-826-509-576	Sequence 576, App
41	122	9.8	1285	4	US-09-016-434-1366	Sequence 1366, Ap
42	120.4	9.7	1233	3	US-09-200-090-1	Sequence 1, Appli
43	120	9.7	1535	3	US-09-668-680-12	Sequence 12, Appl
44	119	9.6	1212	4	US-09-170-496D-113	Sequence 113, App
45	119	9.6	1212	4	US-09-170-496D-223	Sequence 223, App

ALIGNMENTS

RESULT 1  
US-08-993-088A-4  
; Sequence 4, Application US/08993088A  
; Patent No. 6287855  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Sullivan, Kathleen  
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/993,088A  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1...283  
; OTHER INFORMATION: cDNA probe  
US-08-993-088A-4

Query Match 22.8%; Score 283; DB 3; Length 283;  
Best Local Similarity 100.0%; Pred. No. 4.4e-50;  
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCTCCGACCTACTCATCTCTGC 265  
Db 1 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCTCCGACCTACTCATCTCTGC 60

QY 266 TCGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 325  
Db 61 TCGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 120

QY 326 TGTCTGCGGCTGTCCCTCTACCTGTGGGAGAGGCTGCACCTACGCGCTGTCTGCACA 385  
Db 121 TGTCTGCGGCTGTCCCTCTACCTGTGGGAGAGGCTGCACCTACGCGCTGTCTGCACA 180

QY 386 TGACCGCGCTCAGCGTGTGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGTCT 445  
Db 181 TGACCGCGCTCAGCGTGTGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGTCT 240

QY 446 TGTACCGCGCGCGCTTCCGCGCGCTCAGCTGTCTCTG 488  
Db 241 TGTACCGCGCGCGCTTCCGCGCGCTCAGCTGTCTCTG 283

## RESULT 2

US-08-993-424B-4  
; Sequence 4, Application US/08993424B  
; Patent No. 6337206  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Kolakowski, Lee F., Jr.  
; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/993,424B  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846NP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1...283  
; OTHER INFORMATION: cDNA probe

## US-08-993-424B-4

Query Match 22.8%; Score 283; DB 3; Length 283;  
Best Local Similarity 100.0%; Pred. No. 4.4e-50;  
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCTCCGACCTACTCATCTCTGC 265  
Db 1 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCTCCGACCTACTCATCTCTGC 60

QY 266 TCGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 325  
Db 61 TCGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 120

QY 326 TGTCTGCGGCTGTCCCTCTACCTGTGGGAGAGGCTGCACCTACGCGCTGTCTGCACA 385  
Db 121 TGTCTGCGGCTGTCCCTCTACCTGTGGGAGAGGCTGCACCTACGCGCTGTCTGCACA 180

QY 386 TGACCGCGCTCAGCGTGTGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGTCT 445  
Db 181 TGACCGCGCTCAGCGTGTGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGTCT 240

QY 446 TGTACCGCGCGCGCTTCCGCGCGCTCAGCTGTCTCTG 488  
Db 241 TGTACCGCGCGCGCTTCCGCGCGCTCAGCTGTCTCTG 283

## RESULT 3

US-09-603-680-4  
; Sequence 4, Application US/09603680  
; Patent No. 6544753  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Sullivan, Kathleen  
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/603,680  
; FILING DATE: 26-Jun-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; APPLICATION NUMBER: 08/993,088  
; FILING DATE: 18-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846 CA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other

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FEATURE:
; NAME/KEY: Other
; LOCATION: 1...283
; OTHER INFORMATION: cdna probe
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-603-680-4

Query Match      22.8%; Score 283; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.4e-50;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      206  TCGCGACCAACCACCAACTGTGTACCTGGCGCAGCATGGCGGTGCCGACTACTCATCTCTGC 265
Db      1   TCGCGACCAACCACCAACTGTGTACCTGGCGCAGCATGGCGGTGCCGACTACTCATCTCTGC 60

Qy      266  TCGGGCTGCGGTTCGACCTGTACCGCCCTCGCGCGCTCGCGGCCGTGGGTGTTTCGGGGCCGC 325
Db      61  TCGGGCTGCCGTTCGACCTGTACCGCCCTCGCGCGCTCGCGGCCCTCGGGGTGTTTCGGGGCCGC 120

Qy      326  TGCTCTGCGCGCTGTGCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGTCTGCACA 385
Db      121  TGCTCTGCGCGCTGTGCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGTCTGCACA 180

Qy      386  TGACCGGCGCTCAGCGTCGAGCGCTACCTGGCCATCTCGCGCCCGCTCCGCGCCCGCGCT 445
Db      181  TGACCGGCGCTCAGCGTCGAGCGCTACCTGGCCATCTCGCGCCCGCTCCGCGCCCGCGCT 240

Qy      446  TGGTCAACCGGGCGCGCTCGCGCGCTCATCGCTGTGCTGTG 488
Db      241  TGGTCAACCGGGCGCGCTCGCGCGCTCATCGCTGTGCTGTG 283

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RESULT 4
US-09-762-661A-1
; Sequence 1, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1050)
; OTHER INFORMATION: n = A,T,C or G
US-09-762-661A-1

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	Query Match	20.6%;	Score 255.8;	DB 4;	Length 1050;
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Db	56	CGCTGTTCCCGCGCGCTGTGTGGCGGCGTGACGCCACCTGTCGTGGCGCTGTTTCGCGG	115		
Qy	152	TCGGGGTGAGCGGGCAACGTGTGTGACCGTGTACTCTGATCGGGGGCTACCGGGACATGCCGA	211		
Db	116	TGGGCGTTCGGGGCAACCTGTTGACGGTGTCTGTGTGTGCGGGCTTTCGCGAGCTGCACA	175		

Qy	212	CCACCACCAACTGTGTACCTTGGGAGCAGATGGCCGTGTCCGACCTTACATCTCTGCTCGGGC	271
Db	176	CCACCACCAACTGTGTACCTTGGAGCGTGGCCCTGCTCCGACCTGCTCATCTTCTGTGCA	235
Qy	272	TGCGCTTCGACCTGTACCGCCTCTGGCGCTCGCGGCCCTGSGGTGTCGGGCCGCTGCTCT	331
Db	236	TGCGCTCGACCTGTGTGCGCTGTGGAGGTACCGGCCCTGGACCTTTCGGGGAACCTGCTCT	295
Qy	332	GCGCCCTGTCCCTCTAAGTGGGCGAGGGCTGCACTACGCCACGCTGCTGCACATGACCG	391
Db	296	GCAAACTCTTCCAGTTCTGTGAGCGAGGGCTGCACCTACGCCACGGTCTCACCATCACGG	355
Qy	392	CGCTCAGCGTGGAGCGGTACTTGGCCATCTGCGCGCGGCTTCGGGCCCGGCTTGTGTC	451
Db	356	CGCTGAGCGTGGAGCGGTACTTGGCCATCTGCTTCCCGCTTCGCGGCCCAAGGTGCTGTGA	415
Qy	452	CCGGCGCCCGCTTCGCGCGCTCATCGCTGTGCTCTGGGCGGTGGGCGCTGCTCTGCGCG	511
Db	416	CCAAGGGCCGCTGAAGCTGGCCCTGCTGSCATCTGGGCGGTGGCTTCTGAGCGCGCG	475
Qy	512	GTCCCTTTTGTTCCTGTGTGGGCGTGGAGCAGACCCCGGCATCTCCGTAGTCCCGGGCC	571
Db	476	GGCCCATCTTCTGTGTGTGGGCGTGGAGCAGAGAACGGCACG-----	519
Qy	572	TCATGGCACCGCGGATCGCTCTCGCCTCTCGCCTCTCGCGCCTCTCTGGCTCT	631
Db	520	-----GACCC	524
Qy	632	CGCGGGCGCCACCGCGCTCCCGCGTGGGGCCCGAGACCGCGAGGCGCGCGCTGT	691
Db	525	CCGGGACACCGGAGTGGCGCGCCACCGAGTTG-----	559
Qy	692	TCAGCCCGGAATGCCGGCCGAGCCCGCGCAGTGGGCGCTGCGTGTGTCATGCTGTGGG	751
Db	560	-----CGTGGCTCGGGCTGCTCAGGCCATGCTGTGGG	595
Qy	752	TCACCACCGCTACTTCTTCTGCCCTTCTGTGCTCAGCATCTCTACGGGCTCATCG	811
Db	596	TGTCCAGCGTCTTCTTCTTCTGCCGTCTTCTGCTCAGCGTCTCTACGGCTCATCG	655
Qy	812	GGCGGAGCTGTGGAGCAGCGCGCGCTGGCGGCCCGCGCTCGGGGCGGAG	871
Db	656	GCAGGAAGCTGTGGCGCGGGGCGCGGCACACNGGGGGGCGCTCGCTCCGCGAGC	715
Qy	872	GAGGCACCGGCAGACCGTCCGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	931
Db	716	AGAGCCACCGGCAGACCGGTGAAGATGCTCGCTGTGCTGTGTGTGTGTGTGTGTGTGT	775
Qy	932	GTTTGGCTTCCAGTTGGCAGA-----ATCATTTACATAAACACGGAAGATTGCG	982
Db	776	GGCTGCCCTTCCAGTGGGGCGATATTTATTTCCAAAGTCTTCGAGCCCGGCTCTGG	835
Qy	983	GGATGATGTACTTCTCTCAGTACTTTAAACATCGTGTGCTGCAACTTTTCTATCTGAGCG	1042
Db	836	AGATTGCTCAGATCAGCAATACTGCAACCTGGTATCTTTTGTCTCTTCTACCTCAGTG	895
Qy	1043	CATCTATACCCAACTCTTACAACTCATTTCAAAGAGTACAGAGCGCGGCCCTTTA	1102
Db	896	CTGCCATCAATCCATTTCTGTACAAATCATGTCTCAAGAAAGTACCGGGTGGCGGTGTCTCA	955
Qy	1103	AACTGTGTG 1110	
Db	956	AGTTCTG 963	

RESULT 5

US-09-077-675A-1

; Sequence 1, Application US/09077675A

; Patent No. 6242199

; GENERAL INFORMATION:

; APPLICANT: Pai, Lee-Yuh

; APPLICANT: Feigner, Scott C.



Db 249 TGCCTCCGACCTCTTCGCGCTCTCGCAGTACCGGCTTGGAACTTGGCAACCTGCTCT 308  
Qy 332 GCGGCTGTCCCTCTACGTGGCGAGGGCTGCACCTAGCCACGCTGCTGCACATGACCG 391  
Db 309 GCAAACTCTTCCAGTTGTTAGCGAGAGTGCACCTACGCCACAGTGTCTCACCATCACG 368  
Qy 392 GCGTCAGGCTGAGCGCTACCTGGCCATCTGCGGCCGCTGCGGCCGCGCTTGTGTCA 451  
Db 369 CGCTGAGGCTGAGCGCTACTTCGCCATCTGCTTCCGCTGCGGCCCAAGGTAGTGTCA 428  
Qy 452 CCGGCGCGCGCTCGCGCGCTCATCGCTGTGCTCTGGCGCGTGGCGCTGCTCTGCGG 511  
Db 429 CCAAGGCGGGTAAAGCTGTCTGCTCATCTGGCCCTGGCCCTTCTGACGCGCG 488  
Qy 512 GTCCCTTCTGTCTGCTGGCGCTGAGCAGGACCCCGCA 553  
Db 489 GCGCCATCTTCTGTGCTGGTGGAGTGGAGCATGATAACGGCA 530

## RESULT 7

US-09-743-475-2

; Sequence 2, Application US/09743475

; Patent No. 6682908

; GENERAL INFORMATION:

; APPLICANT: Smith, Roy G.

; APPLICANT: Van der Ploeg, Leonardus H. T.

; APPLICANT: Howard, Andrew D.

; APPLICANT: Zheng, Hui

; APPLICANT: McKee, Karen Kulju

; APPLICANT: Jiang, Michael M.

; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE

; FILE REFERENCE: 20218P

; CURRENT APPLICATION NUMBER: US/09/743,475

; PRIOR FILING DATE: 2001-01-10

; PRIOR APPLICATION NUMBER: PCT/US99/15375

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: 60/092,361

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1095

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-743-475-2

Query Match 18.7%; Score 231.6; DB 4; Length 1095;  
Best Local Similarity 68.8%; Pred. No. 3.le-39;  
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 92 GCGCCTTTCCCTGGGGCGCTGGTGGCGGTGACCGCTGTGTGCGCTGCTGCTGCTGCTG 151  
Db 104 CACTGTTCCCGCGCGCTGCTGGCGGGGTCACTGCCACCTGCGTGGCGCTCTTCGTGG 163  
Qy 152 TCGGGGTGAGCGGCAACCTGTGACCGTGTGATCGGGCGCTACCGGACATGCGGA 211  
Db 164 TGGGCATCTCGGGCAACCTGTCTACCATGTGTGTGCTGCTGCTGCTGCTGCTGCTG 223  
Qy 212 CCACACCAACTTGTACTTGGCAGCATGGCGGTGCGACCTACTCATCTGCTGCGGC 271  
Db 224 CCACACCAACTTGTACTTGGCAGCATGGCGGTGCGACCTACTCATCTGCTGCTGCT 283  
Qy 272 TGGCGTTCGACCTGTACCGCTCTGCGCGCTGCGCGCTGCGGTGCTGCGCGCTGCT 331  
Db 284 TGCCGCTGACCTCTGCGCTCTGCGAGTATCGGCCCTTGGAACTTGGCGACCTGCTCT 343  
Qy 332 GCGGCTGTCCCTCTACGTGGCGAGGGTGCACCTAGCCACGCTGCTGCACATGACCG 391  
Db 344 GCAAACTCTTCCAGTTTGTACGAGAGTGCACCTAGCCACGCTCTCACCATCACCG 403  
Qy 392 CGCTCAGGCTGAGCGCTACTTGGCCATCTGCGGCCGCTGCGGCCGCGCTTGTGTCA 451

Db 404 CGCTGAGGCTCGAGGGCTACTTCGCCATCTCTCCCGCTCGGGGCCAAGGTGTTGTCA 463  
Qy 452 CCCGCGCGCGCTCCGCGCGCTCATCGCTGTGCTCTGGCGCGTGGCGCTGCTCTCTGCGG 511  
Db 464 CCAAGGCGCGTGTGAAGCTGTCTTGTGTATCTGGCGCTGGCTTCTGACGCGCGG 523  
Qy 512 GTCCCTTCTTCTTCTGCTGGCGCTGAGCAGGACCCCGGCA 553  
Db 524 GCGCCATCTTCTGCTGCTGGCGCTGGAGCAGAGAACGGCA 565

## RESULT 8

US-09-743-475-1

; Sequence 1, Application US/09743475

; Patent No. 6682908

; GENERAL INFORMATION:

; APPLICANT: Smith, Roy G.

; APPLICANT: Van der Ploeg, Leonardus H. T.

; APPLICANT: Howard, Andrew D.

; APPLICANT: Zheng, Hui

; APPLICANT: McKee, Karen Kulju

; APPLICANT: Jiang, Michael M.

; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE

; FILE REFERENCE: 20218P

; CURRENT APPLICATION NUMBER: US/09/743,475

; PRIOR FILING DATE: 2001-01-10

; PRIOR APPLICATION NUMBER: PCT/US99/15375

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: 60/092,361

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 4009

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-743-475-1

Query Match 18.7%; Score 231.6; DB 4; Length 4009;  
Best Local Similarity 68.8%; Pred. No. 4e-39;  
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 92 GCGCCTTTCCCTGGGGCGCTGGTGGCGGTGACCGCTGTGTGCTGCTGCTGCTGCTGCTG 151  
Db 605 CACTGTTCCCGCGCGCTGCTGGCGGCGTCACTGCCACCTGCGTGGCGCTCTTCGTGG 664  
Qy 152 TCGGGGTGAGCGGCAACCTGTGACCGTGTGATCGGGCGCTACCGGACATGCGGA 211  
Db 665 TGGGCATCTCGGGCAACCTGTCTACCATGTGTGTGCTGCTGCTGCTGCTGCTGCTG 724  
Qy 212 CCACACCAACTTGTACTTGGCAGCATGGCGGTGTCGACCTACTCATCTGCTGCTGCTG 271  
Db 725 CCACACCAACTTGTACTTGGCAGCATGGCGGTGTCGATCTGCTCATCTTCTGTCGA 784  
Qy 272 TGGCGTTCGACCTGTACCGCTCTGCGCGCTCGCGGCCCTGGGTGTTGCGGCGCTGCTCT 331  
Db 785 TGCGCGTGGACCTCGTCCGCTCTGGCAGTATCGGCCCTTGAACTTGGCGACCTGCTCT 844  
Qy 332 GCGGCTGTCCCTCTAGTGGGCGAGGCTGCACCTAGCCACGCTGCTGCACATGACCG 391  
Db 845 GCAAACTCTTCCAGTTTGTACGAGAGCTGCACCTAGCCACGCTCTCACCATCACCG 904  
Qy 392 CGCTCAGGCTCGAGCGCTACTTGGCCATCTGCTTCCGCTGCGGCCGCTGCTTGTGTCA 451  
Db 905 CGCTGAGGCTCGAGCGCTACTTGGCCATCTGCTTCCGCTGCGGCCGAGGTGTTGTCA 964  
Qy 452 CCCGCGCGCGCTCCGCGCGCTCATCGCTGTGCTCTGCGGCCGCTGCGCGCTGCTCTGCGG 511  
Db 965 CCAAGGCGCGTGTGAAGCTGTCTTGTGTATCTGGCGCTGGCCCTTCTGACGCGCGG 1024  
Qy 512 GTCCCTTCTTCTTCTGCTGGTGGCGCTCGAGCAGGACCCCGGCA 553

Db 1025 GCGCCATCTTCGTGCTGGTGGCGGTGGAGCAGGACGCGCA 1066

## RESULT 9

US-09-077-675A-4  
; Sequence 4, Application US/09077675A  
; Patent No. 6242199  
; GENERAL INFORMATION:  
; APPLICANT: Pai, Lee-Yuh  
; APPLICANT: Feigner, Scott C.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Pong, Sheng-Shung  
; APPLICANT: Van Der Ploeg, Leonardus H.T.  
; TITLE OF INVENTION: RECEPTOR ASSAY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,675A  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19590P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1029 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-09-077-675A-4

Query Match 18.6%; Score 230; DB 3; Length 1029;  
Best Local Similarity 68.6%; Pred. No. 6.5e-39;  
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 92 CGCCCTTTCCCTGGGGCGGTGGTGGCGGTGGAGCAGGACGCGCA 151  
Db 266 CGCTCTTCCCAACGCGCTGTGGCGGGCGTCAACGCGACCTGGCGCTTTCGTGG 325

QY 152 TCGGGGTGAGCGGCAACGTGGTGGACCGTGTGATCGGGCGCTACCGGACATGCGGA 211  
Db 326 TGGGTATCGCGGGCAACCTGTCTACGATGCTGGTAGTGTACGCTTCGCGGAGATGCGCA 385

QY 212 CCACCACCAACTGTACCTGGGCGATGGCGGTGTCGACCTACTCATCTGCTCGGGC 271  
Db 386 CCACCACCAACTGTACTGTCCAGATGGCGCTTCTCCGAACCTACTCATCTCTGCA 445

QY 272 TGCCGTTGCACTGTACCGCTCTCGCGCTCGCGCGCTGGGTGTTCGGGCGCGTGTCT 331  
Db 446 TGCCCTCGAACTCTTCGCGCTTTGGCAGTACCGGCTTGGAACTTGGCAACCTGCTCT 505

QY 332 GCGGCTTCCCTCTACGTGGGCGAGGCTGCACTAGCCACGCTGTCGACATGACCG 391

Db 506 GCAAACTTTCAGTTCGTTAGCGAGAGCTGCACCTAGCCACAGTGTCTACCATCACCG 565

QY 392 CGCTCAGGTGAGCGGTACCTGCGCATCTGCGCGCGCTCGCGCGCGCTCTTGCTCA 451  
Db 566 CGCTGAGCGTGCAGCGCTACTTCGCCATCTCTCCCGCTCGCGGCGCAAGGTAGTGTCA 625

QY 452 CCCGCGCGCGGTCCGCGCGCTCATCGTGTGCTCTGGGCGCTGGCGCTGCTCTCTGCGG 511  
Db 626 CCAAGGCGCGGTAAAGCTGGTCACTCTGGTCACTGGGCGCTGGCCCTTCTGCGAGCGCG 685

QY 512 GTCCCTTCTTCTTCTGCTGGTGGCGTGGAGCAGGACCGCGGCA 553  
Db 686 GCGCATCTTCGTGCTGGTGGAGTGGAGCATGATAACGCA 727

## RESULT 10

US-09-077-674-4  
; Sequence 4, Application US/09077674  
; Patent No. 6531314  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris E.  
; APPLICANT: Feigner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,674  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19589P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1029 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-09-077-674-4

Query Match 18.6%; Score 230; DB 4; Length 1029;  
Best Local Similarity 68.6%; Pred. No. 6.5e-39;  
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 92 CGCCCTTTCCCTGGGGCGGTGGTGGCGGTGGAGCAGGACGCGCA 151  
Db 266 CGCTCTTCCCAACGCGCTGTGGCGGGCGTCAACGCGACCTGGCGCTTTCGTGG 325



152	Qy	TCGGGGTGAGCGGCAACGTGTGACCGGTGATGCTGATCGGGCGCTACCGGGACATCGGCA	211
326	Db	TGGGTATCGCGGGCAACCTGCTTACGATGCTGGTAGTGTACACGCTTCCGGAGATCGCA	385
212	Qy	CCACCACCAACCTTGTACCTTGGGCAGCATGGCCGTGTCGGACCTACTCATCTCGCTCTCGGGC	271
386	Db	CCACCACCAACCTTAACTGTCCAGATGGGCTTCTTCGAACTACTCATCTTCTCTGCA	445
272	Qy	TGCGGTTTCGACCTGTACCGCTCTTGCGCGCTTCGCGGCCCTGGGTGTTGCGGCCGCTCTCT	331
446	Db	TGCCCCTCGAACCTCTTCCGCTTTGGCAGTACCGGCTTGGAACTTGGCAACTCTCTCT	505
332	Qy	GCGCGCTGTCCCTCTACGTGGCGAGGGCTGCACCTAGCGCACTGCTGCTGCACATGACCG	391
506	Db	GCAAACTCTTCCAGTTCGTTAGCGAGAGCTGCACCTACGCCACAGTGTCTCACCATCACCG	565
392	Qy	CGCTCAGCGCTGAGCGCTACCTTGGGCATCTCCGCCCGCTCCGGCCCGGGTCTTGGTCA	451
566	Db	CGCTGAGCGTCCGAGCGCTACTTTCGGCCATCTGCTTCCCGCTTCGGGGCCAGGTAGTGTCA	625
452	Qy	CCGGCGCGCGCTCCGCGCGCTCATTCGCTGTGCTCTCGGGCCGTGGCGCTGCTCTCTGCGCG	511
626	Db	CCAAAGGCGCGGTAAAGCTGTGTCATCTCGGTTCATCTGGGCGGTGGCCCTTCTGCA	685
512	Qy	GTCCCTTCTTGTCTCTGTTGGCGCTGAGCAGGACCCCGGCA	553
686	Db	GGCCCATCTTCTGCTGTGTTGTCGAGGTGAGCATGATAACGGCA	727

RESULT 11

```

US-09-077-675A-15
; Sequence 15, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Fong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1092 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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Db 941 CTGCCATCAACCCCATCTGTACAAACATCATGTCTCAGAGAGTACCGGTGGCAGTGTCA 1000  
Qy 1103 AACTGCT 1109  
Db 1001 AACTGCT 1007

## RESULT 12

US-09-077-674-15  
; Sequence 15, Application US/09077674  
; Patent No. 6531314  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,674  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19589P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1092 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-077-674-15

Query Match 18.5%; Score 229.8; DB 4; Length 1092;  
Best Local Similarity 57.7%; Pred. No. 7.3e-39;  
Matches 593; Conservative 0; Mismatches 302; Indels 132; Gaps 5;

Qy 92 GCCTCTTCCCTGGGGCGCTGGTGGCGGTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGCG 151  
Db 104 CGCTGTTCCCGCTCGCTGTGGCAGGCTACCGCCACCTGCTGGCGGTCTCTCGTG 163  
Qy 152 TGGGGGTGAGCGGCAACGTGTGACCGCTGATCGGGCGCTACCGGACATGCGGA 211  
Db 164 TGGGATCTCAGGCAACCTGCTCACTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 223  
Qy 212 CCACCAACACTGTACTTGGGACGATGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271  
Db 224 CCACCAACACTGTACTTGGGACGATGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283

Qy 272 TGCGGTTTCGACCTGTACCGCTCTGGCGCTCGCGCCCTGGGTGTTCGGGCGCGTGTCT 331  
Db 284 TGCGGCTGGACCTCGTCCGCTCTGGCAGTACCGGCTTGAACCTTCGGGACCTGCTCT 343  
Qy 332 GCCGCTGTCCCTCTACGTGGGCGAGGCTGCACTACGCCACGCTGTGCACATGACCG 391  
Db 344 GCAAACTCTTCAGTGTGTGTCAGCGAGAGCTGCACTACGCCACGCTCTACCATCACCG 403  
Qy 392 CGCTCAGGTCGAGGCTACTGTGCGCATCTGCCCGCGCTCCGCGCGCGCTGTGCTGCA 451  
Db 404 CGCTGAGCGTCGAGCGCTACTTCCCATCTGCTTCCCTCTGCGGGCCAAAGTGTGGTCA 463  
Qy 452 CCCGCGCGCGCTCCGCGCGCTCATCTGCTGTGCTCTGGGCGGTGGCGCTGCTCTGTGCG 511  
Db 464 CTAAGGGCGCGGTGAAGCTGTGTCTGTCTGTCATCTGGCGCTGGCTTCTTGCAGCGGG 523  
Qy 512 GTCCCTTCTTGTCTCTGCTGGGCGTTCAGAGAGAGACCGCGGATCTCCGTAGTCCGGGCC 571  
Db 524 GGCCCATCTTGTGCTGTGGGCGTGGAGCAGCAAAACGGCA----- 565  
Qy 572 TCAATGGCACCGCGGAGTCCGCTCTCTGCGCTCTGCTGCGCGCTCTCTGCGCTCT 631  
Db 566 -----CAGATCC 572  
Qy 632 CGCGGGCGCCACCGCGCTCCCGCGCTCGGGGCGCGAGACCGCGAGCGCGCGGCTGT 691  
Db 573 CCGGACACCAACGAATGCCGCGC-----ACCGAGTTCGCTGTGGCTCTGGGCTGC 625  
Qy 692 TCAGCCCGGAATGCCGCGGAGCCCGCGAGCTGGGCGCGCTCGGTGTCTGCTGTGGG 751  
Db 626 TCACC-----GTCAATGGTGGG 643  
Qy 752 TCACACCGCTACTTCTTCTGCGCTTCTGTCGCTCAGCATCTCTACGGGCTCATCG 811  
Db 644 TGTCCAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 703  
Qy 812 GCGGAGAGCTGTGGAGCAGCGCGCGCTGTCAGAGCGCGCGCTCGGGGCGGAGAGA 871  
Db 704 GGAGGAAGCTATGCGGAGAGCGG---AGATGAGCGGTGGCGCGCTCGCTCCGGGACC 760  
Qy 872 GAGGCGACCGGACACCGTCCGCTCTGCTGTGGTGTGGTGTGCTGCTGCTGCTGCTGCT 931  
Db 761 AGAACCAACAGCAGACAGTGAAGATGCTGTGCTGTGGTGTGCTTCTTCTTCTTCT 820  
Qy 932 GGTTCGCTTCCAGTGTGGCAGATCATTTACATAAACAACGAGATTCGCGGATGATGT 991  
Db 821 GGCTGCGCTTCCAGTGTGGGAGATACCTCTTTTCCAGTCTTTCGAGCTGCTCTCTGG 880  
Qy 992 ACTTCTCT-----CAGTACTTTAAACATCGTCTGCTCTGCAACTTTTCTATCTGAGCG 1042  
Db 881 AGATCGCTCAGATCAGCCAGTACTGCAACCTGGTGTCTTGTCTCTTCTTCTTCTCAGCG 940  
Qy 1043 CATCTATCAACCAATCTCTACAACTCATTTCAAGAAGTACAGAGCGCGGCTTTA 1102  
Db 941 CTGCCATCAACCCCATCTGTACAAACATCATGTCCAAAGTACCGGTGGCAGTGTCA 1000  
Qy 1103 AACTGCT 1109  
Db 1001 AACTGCT 1007

## RESULT 13

US-09-016-434-359  
; Sequence 359, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:





	Query Match	100.0%	Score 1239;	DB 15;	Length 1239;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1239;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
Qy	1	ATGGGAGGCCCTTGAACGGGACGACGGCCCCCGAGGGGGCGCGGAGCCGCGCTGGGCC	60		
Db	1	ATGGGAGGCCCTTGAACGGGACGACGGCCCCCGAGGGGGCGCGGAGCCGCGCTGGGCC	60		
Qy	61	GCCTCGCGCCTTGGACAGAGCGCGTGTCTCGCCCTTTCCCTTGGGGGGCGCTGGTGGCG	120		
Db	61	GCCTCGCGCCTTGGACAGAGCGCGTGTCTCGCCCTTTCCCTTGGGGGGCGCTGGTGGCG	120		



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QY 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTACGCCGGAATGCCGCGAGCCCGCG 720
Db 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTACGCCGGAATGCCGCGAGCCCGCG 720
QY 721 CAGCTGGGCGCGCTCGCTGTCATGCTGTTGGTTCACACCGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGCGCTCGCTGTCATGCTGTTGGTTCACACCGCTACTTCTTCTGCGCTTT 780
QY 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCG 840
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCG 840
QY 841 CTGGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCTCGCGTCTG 900
Db 841 CTGGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCTCGCGTCTG 900
QY 901 CTGGTGGTGGTCTGGCAATTAATTTGCTGGTTGCCCTTCCAGTTGGCAGATCAAT 960
Db 901 CTGGTGGTGGTCTGGCAATTAATTTGCTGGTTGCCCTTCCAGTTGGCAGATCAAT 960
QY 961 TACATAAACAAGGAGATTTCGGGATGATGATCTCTCTCAGTACTTTTAAACATCGTCT 1020
Db 961 TACATAAACAAGGAGATTTCGGGATGATGATCTCTCTCAGTACTTTTAAACATCGTCT 1020
QY 1021 CTGCAACTTTTCTATCTAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080
Db 1021 CTGCAACTTTTCTATCTAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080
QY 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTCGCAAGGAAGTCCAGGCGGAGGCTTC 1140
Db 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTCGCAAGGAAGTCCAGGCGGAGGCTTC 1140
QY 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGCGGGGACACTGGAGGAGACACGTTGGC 1200
Db 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGCGGGGACACTGGAGGAGACACGTTGGC 1200
QY 1201 TACACCGAGACAGCGCTAACTGAAGACGATGGATAA 1239
Db 1201 TACACCGAGACAGCGCTAACTGAAGACGATGGATAA 1239
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## RESULT 3

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US-10-290-078-14
; Sequence 14, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE OF INVENTION: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MPI2001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-290-078-14
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Query Match 100.0%; Score 1239; DB 15; Length 1239;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGGCGAGCCCTGGAAACGCGAGCGACGCGCCCGGAGGCGCGGAGCGCGGCGCC 60
Db 1 ATGGGCGAGCCCTGGAAACGCGAGCGACGCGCCCGGAGGCGCGGAGCGCGGCGCC 60
QY 61 GCGCTGCCGCTTGGAGCAGCGCGCTGCTCGCCCTTTCCCTCGGGGCGCTGGTGGCG 120
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Db 61 GCGCTGCCGCTTGGAGCAGCGCGCTGCTCGCCCTTTCCCTCGGGGCGCTGGTGGCG 120
QY 121 GTGACCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GTGACCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 ATGTGATCGGGCGCTACCGGGAATGCGGGAACACCAACCTTGTACCTGGGAGCATG 240
Db 181 ATGTGATCGGGCGCTACCGGGAATGCGGGAACACCAACCTTGTACCTGGGAGCATG 240
QY 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 TCGGCGCGCTCGGTGTTTCGGGCGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTG 360
Db 301 TCGGCGCGCTCGGTGTTTCGGGCGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTG 360
QY 361 TGCACCTACGCAACGCTGCTGCAATGACCGCGCTCAGCGTGCAGCGCTACCTGGCCATC 420
Db 361 TGCACCTACGCAACGCTGCTGCAATGACCGCGCTCAGCGTGCAGCGCTACCTGGCCATC 420
QY 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GTGCTCTGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 GTGCTCTGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 CAGAACCCGCGCATCTCCGTAAGTCCCGGCTCAATGAGCAACCGCGGATCGCTTCCTG 600
Db 541 CAGAACCCGCGCATCTCCGTAAGTCCCGGCTCAATGAGCAACCGCGGATCGCTTCCTG 600
QY 601 CCTCTCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 CCTCTCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTACGCCGGAATGCCGCGAGCCCGCG 720
Db 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTACGCCGGAATGCCGCGAGCCCGCG 720
QY 721 CAGTGGGCGCGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 CAGTGGGCGCGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCG 840
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCG 840
QY 841 CTGGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCTCGCGTCTG 900
Db 841 CTGGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCTCGCGTCTG 900
QY 901 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 TACATAAACAAGGAGATTTCGGGATGATGATCTCTCTCAGTACTTTTAAACATCGTCT 1020
Db 961 TACATAAACAAGGAGATTTCGGGATGATGATCTCTCTCAGTACTTTTAAACATCGTCT 1020
QY 1021 CTGCAACTTTTCTATCTAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080
Db 1021 CTGCAACTTTTCTATCTAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAAG 1080
QY 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTGCTCGCAAGGAAGTCCAGGCGGAGGCTTC 1140
Db 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTGCTCGCAAGGAAGTCCAGGCGGAGGCTTC 1140
QY 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGCGGGGACACTGGAGGAGACACGTTGGC 1200
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Qy	1	ATGGGAGCCCTTGGAAACGGCAGCGACGGCCCGAGGGGGCGCGGAGCGCCGCTGGCCCC	60
Db	1	ATGGGAGCCCTTGGAAACGGCAGCGACGGCCCGAGGGGGCGCGGAGCGCCGCTGGCCCC	60
Qy	61	GGCTCCGCGCTTGGCAAGCAGCGCGCTGCTCGCCCTTTCCCTGGGGGCGCTGTGTGCGG	120
Db	61	GGCTCCGCGCTTGGCAAGCAGCGCGCTGCTTGCCCTTTCCCTTGGGGGCGCTGTGTGCGG	120
Qy	121	GTGACCGCTGTGTGCTGTGCTGTTCGTCTGGGGTGAGCGGCACACTGTGTGACCGGTG	180
Db	121	GTGACCGCTGTGTGCTGTGCTGTTCGTCTGGGGTGAGCGGCACAACTGTGTGACCGGTG	180
Qy	181	ATGCTGATCGGGGGCTACCGGGACATCGGGACCAACCACCACTTGTACTCTGGGACGATG	240
Db	181	ATGCTGATCGGGGGCTACCGGGACATGCGGGACCAACCACCACTTGTACTTGGGACGATG	240
Qy	241	GCGGTGTCCGACCTACTCTCATCTGTCTGGGGCTGCCCTTCGACCTGTACCGCCCTCTGGCGC	300
Db	241	GCGGTGTCCGACCTACTCTCATCTGTCTGGGGCTGCCCTTCGACCTGTACCGCCCTCTGGCGC	300
Qy	301	TGCGGCGCCCTGGGTGTTTGGGGCGCGTGTCTGTGCGGCTGTCTCTCTTACTGTGGGCGAGGCG	360





QY 721 CAGCTGGGCGCGCTCGTGTGATGCTGGGTGACACCGCTACTTCTTCTGCGCCCTT 780  
Db 721 CAGCTGGGCGCGCTCGTGTGATGCTGGGTGACACCGCTACTTCTTCTGCGCCCTT 780  
QY 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGAGAGCGCGCGCG 840  
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGAGAGCGCGCGCG 840  
QY 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCGCGCGCGCGCGCGCGCTG 900  
Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCGCGCGCGCGCGCGCGCTG 900  
QY 901 C 901  
Db 901 C 901

RESULT 9  
US-10-723-955-129  
; Sequence 129, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinsma, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US29.CON  
; CURRENT APPLICATION NUMBER: US/10/723,955  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 10/417,820  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 129  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-955-129

Query Match 72.3%; Score 896.2; DB 18; Length 2040;  
Best Local Similarity 99.7%; Pred. No. 6.4e-234;  
Matches 898; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGGGAGCCCTTGGAAACGGACCGACCGCCCGAGGGCGCGGAGCGCCCGTGGGCC 60  
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Db 1 ATGGGAGCCCTTGGAAACGGACCGACCGCCCGAGGGCGCGGAGCGCCCGTGGGCC 60  
QY 61 GCGTGGCGCGCTCGGACGAGCGCGCTGCTCGGCCCTTTCCCTCGGGGCGCTCGTGGCG 120  
Db 61 GCGTGGCGCGCTCGGACGAGCGCGCTGCTCGGCCCTTTCCCTCGGGGCGCTCGTGGCG 120  
QY 121 GTGACCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Db 121 GTGACCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 181 ATGTGATCGGGCGCTACCGGAGCATCGGAGACCAACCACTTGTACTGGGAGCATG 240  
Db 181 ATGTGATCGGGCGCTACCGGAGCATCGGAGACCAACCACTTGTACTGGGAGCATG 240  
QY 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGCTGACCGCTCTGGGCGC 300  
Db 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGCTGACCGCTCTGGGCGC 300  
QY 301 TCGCGGCGCTGGGTGTTGCGGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 360  
Db 301 TCGCGGCGCTGGGTGTTGCGGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 360  
QY 361 TGCACCTAGCAGCAGCTGCTGACATGACCGCGCTCAGCGTCGAGCGCTACTGGCCATC 420  
Db 361 TGCACCTAGCAGCAGCTGCTGACATGACCGCGCTCAGCGTCGAGCGCTACTGGCCATC 420  
QY 421 TCGCGGCGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 421 TCGCGGCGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 GTGCTCTGGGCGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 481 GTGCTCTGGGCGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
QY 541 CAGGACCCCGCATCTCGGTAGTCGCGGCGCTCAATGGCACCGCGCGATCGCTCTCTCG 600  
Db 541 CAGGACCCCGCATCTCGGTAGTCGCGGCGCTCAATGGCACCGCGCGATCGCTCTCTCG 600  
QY 601 CCTCTCGGCTCGTGGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 601 CCTCTCGGCTCGTGGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
QY 661 GGGCCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 661 GGGCCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
QY 721 CAGCTGGGCGCGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 721 CAGCTGGGCGCGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
QY 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCG 840  
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCG 840  
QY 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCGCGCGCGCGCGCGCGCTGCTG 900  
Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCGCGCGCGCGCGCGCGCTGCTG 900  
QY 901 C 901  
Db 901 C 901

RESULT 10  
US-10-417-820A-151  
; Sequence 151, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.

; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled Receptors

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; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-417-820A-151

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Query Match	71.9%; Score 891.4; DB 17; Length 2040;
Best Local Similarity	98.8%; Pred. No. 1.3e-232;
Matches 898; Conservative 0; Mismatches 11; Indels 0; Gaps 0	
QY	1 ATGGGACGCCCTTGAAACGGACGAGCGGCCGAGGGGCGCGGAGACCGCGCTGGGCC 60
DB	
QY	1 ATGGGACGCCCTTGAAACGGACGAGCGGCCGAGGGGCGCGGAGACCGCGCTGGGCC 60
DB	
QY	61 GCGCTGCCGCCCTTGCGACGAGCGCGCTGCTCGGCCCTTTCCCTCTGGGGGCGCTGGTGGCG 120
DB	
QY	61 GCGCTGCCGCCCTTGCGACGAGCGCGCGCTGCTCGGCCCTTTCCCTCTGGGGGCGCTGGTGGCG 120
DB	
QY	121 GTGACCGCTGTGTGCTGTGCTGCTTTCGTGTGGGGTGTAGCGGCAACCTGTGTGTACCGGTG 180
DB	
QY	121 GTGACCGCTGTGTGCTGTGCTGCTTTCGTGTGGGGTGTAGCGGCAACCTGTGTGTACCGGTG 180
DB	
QY	181 ATGTGTATCGGGGCGCTACCGGGACATCGGACCAACCAACCTGTGTGTACCTGGGCGAGCATG 240
DB	
QY	181 ATGTGTATCGGGGCGCTACCGGGACATCGGACCAACCAACCTGTGTGTACCTGGGCGAGCATG 240
DB	
QY	241 GCGGTGTCCGACCTACTCATCTGCTCGGGGTGCGGTTCGACCTGTACCGCTCTCTGGGCGC 300
DB	
QY	241 GCGGTGTCCGACCTACTCATTAATGCTCGGGGTGCGGTTCGACCTGTACCGCTCTCTGGGCGC 300
DB	
QY	301 TCGGGGCCCTTGCGGTGTTGGGCGCGCTGCTGTGCGCGCTGTTCCTCTACGTGGGCGAGGCG 360
DB	
QY	301 TCGGGGCCCTTGCGGTGTTGGGCGCGCTGCTGTGCGCGCTGTTCCTCTACGTGGGCGAGGCG 360
DB	
QY	361 TGCACCTACGCCACGCTGTGCATACCGCGCTCAGCGTGTAGCGGCTACTCTGGCCATC 420
DB	
QY	361 TGCACCTACGCCACGCTGTGCATACCGCGCTCAGCGTGTAGCGGCTACTCTGGCCATC 420
DB	
QY	421 TGCGCCCGGCTCTCGGCGCCGGCTCTTGGTCAACCGCGCGCGCTCGCGCGCTCATCGCT 480
DB	
QY	421 TGCGCCCGGCTCTCGGCGCCGGGTCTTGGTCAACCGCGCGCGCTCGCGCGCTCATCGCT 480
DB	
QY	481 GTGCTCTGGGCGGTGGCGTCTCTCTGCCGGTCCCTTTCTTGTTCCTGTGTGGGCGTGCAG 540
DB	
QY	481 GTGCTCTGGGCGGTGGGCGTCTCTCTGCCGGTCCCTTTCTTGTTCCTGTGTGGGCGTGCAG 540
DB	

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RESULT 11
US-10-363-345A-33737/c
; Sequence 33737, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3'
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33737
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 33737
US-10-363-345A-33737

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Query Match	40.5%	Score	501.2	DB	18	Length	1179
Best Local Similarity	79.9%	Pred.	No. 2.5e-126				
Matches	590	Conservative	0	Mismatches	148	Indels	0
Gaps	0						
1	ATGGGCAGCGCCCTGGAAACGGCAGCGACGGCCCGAGGGGGCGGGAGCGCGGTGCGCC	60					
738	ATAACAACCCCTAAACGACACGACGCGCCCGAAAAACGCGAAACCGCCGTACCC	679					
61	GGCGTCGCGCCTTGGACAGAGCGCGCTGTGTGCGCCCTTTCCCTCTGGGGGCGCTGTGCGCG	120					
678	GGCGTACCGCCTTACGACGAACGCGCGCTACTGTGCGCCCTTTCCCGTAAACACGCTAATACCG	619					
121	GTGACCGCTGTGTGCGCTGTGCGCTTTCTGTCGTGCGGGGTGAGCGGCGAACGTTGGTACCGGT	180					
618	ATAACGGCTATATACCTATACCTATTCTGTCGTAATAATAACGACAAACGTAATAACCGTA	559					
181	ATGCTGATCGGGCGCTTACCGGGAATGCGGAACCAACCAACTTTGTACTCTGGGGGAGCATG	240					
558	ATACTAATCGAAGCGTTACCGAAACATACGAAACCAACCAACCACTTATCTCTTAAACAAACA	499					

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QY 241 GCGGTGTCGACCTACTCATCTCGTGGGCTCGCGTTCGACCTGTACCGCTCTGGGCG 300
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DB 498 ACCGTATCGACCTACTCATCTCGAATACCTACCGTTCGACCTATACCGCTCTAACGC 439
QY 301 TCGGCGCTGGGTGTTTCGGGCGCTGTCTTCGCGGCTGTCTCTTACGTGGGCGAGGC 360
    |||||
DB 438 TCGGACCTAAATATTCGAACCGCTACTCTACCGGCTATCCCTCTACGTAAACGAAAC 379
QY 361 TGCACCTAGCCACCTGTGCACATGACCGGCTCAGGTCGAGCGCTACTTGGCCATC 420
    |||||
DB 378 TACACCTAGCCACCTACTACACATAACCGGCTCAACGTGGAACGCTACCTAACCATC 319
QY 421 TCGCGCGCTCGCGCGCGCTCTTGTGTCACCGCGCGCGTCCGCGCGCTCATCGCT 480
    |||||
DB 318 TACCGCGCGCTCGCGCGCGCTCTTATACCGCGCGCTCGCGCGCTCATCGCT 259
QY 481 GTGCTCTGGGCGCTGTCTCTGCGGCTGTCTCTGCGGCTCTCTTCTTCTGTGGGCGTCGAG 540
    |||||
DB 258 ATACTCTAAACCGTAACGCTACTCTCTACCGATCGCTCTTATTCTTAATAAACGTCGAA 199
QY 541 CAGGACCGCGCATCTCCGTAGTCGCGGCTCAATGGCACCGCGGATCGCTCTCTCG 600
    |||||
DB 198 CAAACCGCGCATCTCCGTAAATCCGAACTCAATAACCGCGGATCGCTCTCTCG 139
QY 601 CCTCTCGCTCTCGCGCGCTCTCTGCTCTCGCGGCGCACCGCGCTCCCGCGCTCG 660
    |||||
DB 138 CTCTCGCTCTCGCGCGCTCTCTAACTCTCGCGAACGCGCGCTCCCGCGCTCG 79
QY 661 GGGCGCGGAGACCGCGGAGCGCGGCTGTTCAGCGCGGAATCGCGCGGAGCGCGCG 720
    |||||
DB 78 AAACCGGAAACCGGAAACCGCGAGCTATTCAACCGCGAATACCGACCGAAACCGCG 19
QY 721 CAGCTGGGCGCGCTCGT 738
    |||||
DB 18 CAACTAACCGCGCTACGT 1

RESULT 12
US-10-363-345A-33738
; Sequence 33738, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33738
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 33738
US-10-363-345A-33738

Query Match 40.5%; Score 501.2; DB 18; Length 1179;
Best Local Similarity 79.9%; Pred. No. 2.5e-126;
Matches 590; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 1 ATGGGACGCCCCCTGGAACGCGACGCGCCCCCGAGGGGCGGGAGCGCGGTGGCCC 60
    |||||
DB 442 ATAACAAACCCCTTAAACGACACACGACCGCCCCGAAAAACGCGCGTAACCC 501
QY 61 GGGCTCGGCTTGGACGAGCGCGCTGTCTGCCCTTTTCCCTTGGGGCGCTGTGGCG 120
    |||||
DB 502 GGGCTACCGCTTACGACGACGCGCTACTCGCCCTTTCCCTTAAACGCTAATACG 561
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QY 121 GTGACGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
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DB 562 ATAACCGCTATATACCTATACCTATTCGTCGTAATAAAGCAACGTAATAACCGTA 621
    |||||
QY 181 ATGTGATCGGGCGCTACCGGACATGGGACACCAACCACTTGTACTCTGGGAGCATG 240
    |||||
DB 622 ATACTAATCGAACGCTACCGAAACATAGAACCAACCACTTATATCTAAACAAATA 681
    |||||
QY 241 GCGGTGTCGACCTACTCATCTCGTGGGCTGGCGTTCGACCTGTACCGCTCTGGGCG 300
    |||||
DB 682 ACCGTATCGGACCTACTCATCTCGAATACCGTTCGACCTATACCGCTCTAACGC 741
    |||||
QY 301 TCGGCGCTGGGTGTTTCGGGCGCTGTCTTCGCGGCTGTCTCTTCTAGTGGGCGAGGC 360
    |||||
DB 742 TCGGACCGCTAAATATTCGAACCGCTACTCTACCGGCTATCCCTCTACGTAAACGAAAC 801
    |||||
QY 361 TGCACCTAGCCACCTGTGCACATGACCGGCTCAGGTCGAGCGCTACTTGGCCATC 420
    |||||
DB 802 TACACCTAGCCACCTACTACACATAACCGGCTCAACGTGGAACGCTACTAACCATC 861
    |||||
QY 421 TCGCGCGCTCGCGCGCGCTCTTGTGTCACCGGCGCGCTCCGCGCGCTCATCGCT 480
    |||||
DB 862 TACCGCGCTCGCGCGCGCTCTTAACTACCGGCGCGCTCCGCGCTCATCGCT 921
    |||||
QY 481 GTGCTCTGGGCGCTGTCTCTGCGGCTGTCTCTGCGGCTCTTCTTGTGCTGGGCGTCGAG 540
    |||||
DB 922 ATACTCTAAACCGTAACGCTACTCTCTACCGATCGCTCTTATTCTTAATAAACGTCGAA 981
    |||||
QY 541 CAGGACCGCGCATCTCCGTAGTCGCGGCTCAATGGCACCGCGGATCGCTCTCTCG 600
    |||||
DB 982 CAAACCGCGCATCTCCGTAAATCCGAACTCAATAACCGCGGATCGCTCTCTCG 1041
    |||||
QY 601 CCTCTCGCTCTCGCGCGCTCTCTGCTCTCGCGGCGCACCGCGCTCCCGCGCTCG 660
    |||||
DB 1042 CTCTCGCTCTCGCGCGCTCTCTAACTCTCGGAAACGCGCGCTCCCGCGCTCG 1101
    |||||
QY 661 GGGCGCGGAGACCGCGGAGCGCGGCTGTTCAGCGCGGAATCGCGCGGAGCGCGCG 720
    |||||
DB 1102 AAACCGGAAACCGGAAACCGCGAGCTATTCAACCGCGAATACCGACCGAAACCGCG 1161
    |||||
QY 721 CAGCTGGGCGCGCTCGT 738
    |||||
DB 1162 CAACTAACCGCGCTACGT 1179
    |||||

RESULT 13
US-10-363-483A-33737/c
; Sequence 33737, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33737
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 33737
US-10-363-483A-33737

Query Match 40.5%; Score 501.2; DB 19; Length 1179;
Best Local Similarity 79.9%; Pred. No. 2.5e-126;
Matches 590; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 1 ATGGGACGCCCCCTGGAACGCGACGCGCCCCCGAGGGGCGGGAGCGCGGTGGCCC 60
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Db 738 ATAACACCCCTTAAAGACAGACCGCGCCCGGAAACCGGAAACCGCGTAAACCC 679  
Qy 61 GCGCTCGCCCTTGGAGAGCGCGCTGCTCGCCCTTTCCCTCGGGGCGTGTGCGC 120  
Db 678 GCGCTACCGCTTACGAGAACCGCGCTACTCGCCCTTTCCCTTAAACCGCTAATACG 619  
Qy 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
Db 618 ATAACCGCTTATACCTATACCTATATTCGTGCTGAAATAAAGCAACAGTAAACCGTA 559  
Qy 181 ATGCTGATCGGGCGGTACCGGACATCGGACACACCACTTCTACTGCGGACGATG 240  
Db 558 ATACTAATGAACCGCTACCGAAACATACGAAACCAACCACTTATATTAACAAACATA 499  
Qy 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGCGGC 300  
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Qy 301 TCGCGCCCTTGGGTGCTGCGGCGCTGTCTGCGCGCTGTCTGCTGCTGCTGCTGCTG 360  
Db 438 TCGCGACCTTAAATATTCGAAACCGCTACTCTACCGCTATCTGCTGCTGCTGCTGCT 379  
Qy 361 TCGACCTAGCCACCGCTGCTGACATGACCGGCTCAGCGTACGAGCGTACTGCGCATC 420  
Db 378 TACACCTAGCCACCGCTACTACACATAACCGGCTCAACGTCGAACTACCTAAACCATC 319  
Qy 421 TCGCGCCCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 318 TACCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259  
Qy 481 GTGCTGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 258 ATACTTAAACCGTAAACGCTACTCTCTACCGTATCTGCTGCTGCTGCTGCTGCTGCT 199  
Qy 541 GAGACCGCGCATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 198 CAAACCGCGCATCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 139  
Qy 601 CCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Db 138 CCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 79  
Qy 661 GGGCCCGAGACCGCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db 78 AAACCGGAAACCGGAAACCGCGAGCTATTCAACCGGGAATACCGACCGAACC CGCG 19  
Qy 721 GAGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738  
Db 18 CAACTAAACCGCGCTACGT 1

## RESULT 14

US-10-363-483A-33738  
; Sequence 33738, Application US/10363483A  
; Publication No. US20050064401A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain  
; TITLE OF INVENTION: illnesses  
; FILE REFERENCE: 82011  
; CURRENT APPLICATION NUMBER: US/10/363,483A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 33738  
; LENGTH: 1179  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: CpG-island No: 33738  
US-10-363-483A-33738

Query Match 40.5%; Score 501.2; DB 19; Length 1179;  
Best Local Similarity 79.9%; Pred. No. 2.5e-126;  
Matches 590; Conservative 0; Mismatches 148; Indels 0; Gaps 0;  
Qy 1 ATGGGCGACCCCTGGAACGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Db 442 ATAAACACCCCTTAAACGACAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 501  
Qy 61 GCGTTCGCGCTTGGACGAGCGCGCTGCTGCGCTTTTCCCTTGGGGCGCTGTGTGCGC 120  
Db 502 GCGTTCGCGCTTGGACGAGCGCGCTGCTGCGCTTTTCCCTTGGGGCGCTGTGTGCGC 561  
Qy 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
Db 562 ATAACCGCTATATACCTATACCTATATTCGTGCTGAAATAAAGCAACAGTAAACCGTA 621  
Qy 181 ATGCTGATCGGGCGGTACCGGACATCGGACCAACCACTTGTACTGGGAGCATG 240  
Db 622 ATACTAATCGAACCGTACCGAAACATACGAAACCAACCACTTATATCTAAACAAACATA 681  
Qy 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGCGGC 300  
Db 682 ACGGTATCGGACCTACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741  
Qy 301 TCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
Db 742 TCGCGACCTTAAATATTCGAAACCGCTACTCTACCGCTATCCCTCTACGTAACGAAAC 801  
Qy 361 TGCACCTAGCCACCGCTGCTGACATGACCGGCTCAGCGTACGCGCTACTGCGCATC 420  
Db 802 TACACCTAGCCACCGCTACTACACATAACCGCGCTCAACGTCGAAACGCTACCTAACCATC 861  
Qy 421 TCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 862 TACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921  
Qy 481 GTGCTGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 922 ATACTTAAACCGTAAACGCTACTCTCTACCGTATCCCTTCTTATCTTAATAACGTCGAA 981  
Qy 541 CAGACCGCGGATCTCGCTAGTCCGGGCTCAATGACCGCGCGGATGCGCTCTCTCG 600  
Db 982 CAAACCGCGGATCTCGCTAGTCCGGGCTCAATGACCGCGCGGATGCGCTCTCTCG 1041  
Qy 601 CCTCTCGCTGCTGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 1042 CCTCTCGCTGCTGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1101  
Qy 661 GGGCCCGAGACCGCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db 1102 AAACCGGAAACCGGAAACCGCGAGCTATTCAACCGGGAATACCGACCGAACC CGCG 1161  
Qy 721 CAGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738  
Db 1162 CAACTAAACCGCGCTACGT 1179

## RESULT 15

US-10-363-345A-33739  
; Sequence 33739, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 33739

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; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 33739
US-10-363-345A-33739

Query Match          35.3%; Score 437.2; DB 18; Length 1179;
Best Local Similarity 74.5%; Pred. No. 6.8e-109;
Matches 550; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 1 ATGGGCAGCCCTGGAAACGGCAGACGCGCCCGAGGGGGCGGAGAGCCGCCGTGGGCC 60
Db 1 ATGGGCAGCCCTGGAAACGGCAGACGCGCCCGAGGGGGCGGAGAGCCGCCGTGGGCC 60
QY 442 ATGGGTAGTATTTTGGAAACGGTAGCATCGTTTCGAGGGGGCGGAGAGTCGTGTTTC 501
Db 442 ATGGGTAGTATTTTGGAAACGGTAGCATCGTTTCGAGGGGGCGGAGAGTCGTGTTTC 501
QY 61 GCGCTGCGCCCTTGGCAGAGCGCGCTGCTGCCCTTTTCCCTCGGGGGCGCTGGTCCG 120
Db 61 GCGCTGCGCCCTTGGCAGAGCGCGCTGCTGCCCTTTTCCCTCGGGGGCGCTGGTCCG 120
QY 502 GCGTTGTCGTTTGGCAGAGCGCTGCTGCCCTTTTCCCTCGGGGGCGCTGGTCCG 561
Db 502 GCGTTGTCGTTTGGCAGAGCGCTGCTGCCCTTTTCCCTCGGGGGCGCTGGTCCG 561
QY 121 GTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 562 GTGATCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 621
Db 562 GTGATCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 621
QY 181 ATGCTGATCGGGCGCTACCGGACATGGGACACACCACTTGTACCTGGGCGAGCATG 240
Db 181 ATGCTGATCGGGCGCTACCGGACATGGGACACACCACTTGTACCTGGGCGAGCATG 240
QY 622 ATGTTGATCGGGCGTTATCGGATATCGGATATTAATTAATTTGTTATTTGGTAGTAG 681
Db 622 ATGTTGATCGGGCGTTATCGGATATCGGATATTAATTAATTTGTTATTTGGTAGTAG 681
QY 241 GCGGTGTCGACCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 GCGGTGTCGACCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 682 GTGCTGTTTCGATTATTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 741
Db 682 GTGCTGTTTCGATTATTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 741
QY 301 TCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 TCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 742 TCGCGGTTTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 801
Db 742 TCGCGGTTTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 801
QY 361 TGCACCTAGCCACGCTGCTGACATGACCGGCTCAGCGTCGAGCGCTACCTGGCCATC 420
Db 361 TGCACCTAGCCACGCTGCTGACATGACCGGCTCAGCGTCGAGCGCTACCTGGCCATC 420
QY 802 TGTATTACGTTACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 861
Db 802 TGTATTACGTTACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 861
QY 421 TCCCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 TCCCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 862 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
Db 862 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
QY 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 922 GTGTTTGGGTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
Db 922 GTGTTTGGGTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
QY 541 CAGGACCCCGGATCTCCGTAAGTCCCGGCTCAATGCAACGCGCGGATCGCCTCCTCG 600
Db 541 CAGGACCCCGGATCTCCGTAAGTCCCGGCTCAATGCAACGCGCGGATCGCCTCCTCG 600
QY 982 TAGGATTTCCGTTATTTTCCGTTTCCGTTTCCGTTTCCGTTTCCGTTTCCGTTTCCG 1041
Db 982 TAGGATTTCCGTTATTTTCCGTTTCCGTTTCCGTTTCCGTTTCCGTTTCCGTTTCCG 1041
QY 601 CCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 CCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 1042 TTTTTCGTTTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101
Db 1042 TTTTTCGTTTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101
QY 661 GGGCCCGGAGACCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 GGGCCCGGAGACCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1102 GGGTTTCGAGATCGCGAGGTCGCGCGCTGTTAGTCGCGAATGTCGTCGAGTTTCGCG 1161
Db 1102 GGGTTTCGAGATCGCGAGGTCGCGCGCTGTTAGTCGCGAATGTCGTCGAGTTTCGCG 1161
QY 721 CAGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 738
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QY 1162 TAGTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1179
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Result No.	Query			DB	ID	Description
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2	230	18.6	4435	3	AX049571	Mus muscu
3	228.4	18.4	688	7	C0959476	AGENCOURT
C 4	227.8	18.4	640	6	C0618070	CB618070 56030361H
5	227.8	18.4	640	6	C0618071	CB618071 56030361J
6	227.8	18.4	1052	9	AY4076564	Hom sapi
7	226.8	18.3	500	2	BF603623	269181 MA
C 8	225.2	18.2	637	6	C0618076	CB618076 56030461H
9	219.2	17.7	608	6	BY724644	BY724644
10	213.6	17.2	969	9	AY4076565	Pan trogl
C 11	203.8	16.4	635	6	C0618069	CB618069 56030353J
C 12	202.2	16.3	576	6	C0618067	CB618067 56030345J
13	193.2	15.6	643	6	C0618077	CB618077 56030461J
14	186.4	15.0	843	5	B0553576	AGENCOURT
15	184.6	14.9	635	6	C0618075	B0553576
16	180.6	14.6	634	6	C0618068	CB618075 56030445J
C 17	174.4	14.1	631	6	C0618073	CB618068 56030353H
C 18	173.4	14.0	849	5	B0568940	CB618073 56030377J
C 19	171	13.8	631	6	C0618074	B0568940
C 20	157.8	12.7	308	9	C3583142	CB618074 56030445H
C 21	150.2	12.1	632	6	C0618066	C3583142
C 22	141.6	11.4	504	8	A2451922	CB618066 56030345H
C 23	134.2	10.8	626	7	C0233556	A2451922 IM0251C06
24	133	10.7	596	6	CB618072	C0233556 523 Full1
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Db 55 CACTGTTCCCGCGCGCTGCTGCGCGCGTCACTGCCACCTGCGTGGCGCTCTTCGTGG 114

Qy 152 TCGGGGTGAGCGGCAACCTGTGACCGTGAAGCTGATCGGGCGGTACCGGACATCGCGA 211

Db 115 TGGGCATCTCGGGCAACCTGTCAACATGCTGGTGGTTCGCCGCTTCGCGAGCTGCGCA 174

Qy 212 CCACCACCAACTGTACCTGGCGACATGGCGGTTCGCGACCTACTCATCTGCTCGCGGC 271

Db 175 CCACCACCAACTGTACCTATCCAGATGGCGCTTTCGAGATGCTCATCTTCCTGTGCA 234

Qy 272 TGCCGTTGCACTGTACCGCTCTCGCGCTCGCGCGCTGCGGTGTCGGCGCGTCTCT 331

Db 235 TGCCGCTGCACTGTGCGCGCTCTGCGAGTATCGCGCTTGGAACTTCGCGACCTGCTCT 294

Qy 332 GCGGCTGCTCTACGTGGCGGAGGCTGCACCTAGCCACGCTGTGTCGACATGACCG 391

Db 295 GCAAACTCTTCAGTTTGTGACGAGAGCTGCACCTAGCCACGCTTCTACCATCACCG 354

Qy 392 CGCTCAGGCTCGAGCGTACCTGCGCATCTGCGCGCGCTCGCGCGCGCTTGGTCA 451

Db 355 CGCTCAGGCTCGAGCGTACTTTCGCGCATCTGCTTCCGCTGCGCGCGCGTGGTCA 414

Qy 452 CCGCGCGCGCTCGCGCGCTCATCGTGTGCTGCGCGCGTGTGCGCTGCTCTGCGCG 511

Db 415 CCAAGGCGGTGTGAAGCTGTGTCATCTGTGTCATCTGCGCGCGTGTGCGCGCGG 474

Qy 512 GTCCCTCTTGTCTGTTGGGCTGCGAGCAGGACCGCGCA 553

Db 475 GCGCCATCTCTGTTGTTGGGCTGCGAGCAGCAGACGCGCA 516

## RESULT 2

AK049671  
LOCUS AK049671 4435 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone: C530020122 product: GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 homolog [Rattus norvegicus], full insert sequence.

ACCESSION AK049671  
VERSION AK049671.1 GI:26340405  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PubMed 10349636

REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PubMed 11042159

REFERENCE  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PubMed 11076861

REFERENCE  
AUTHORS

AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

TITLE  
JOURNAL

## COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>.

FEATURES  
source

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## CDS

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## ORIGIN

Query Match 18.6%; Score 230; DB 3; Length 4435;  
Best Local Similarity 68.6%; Pred. No. 4.4e-39;  
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 92 CGCCCTTCCCTGGGGCGCTGTGCGGTGACCGCTGTGCGCTGTGCTGCTGCTGCG 151

Db 355 CACTGTTCCCGCGCGTCTGGCGGCGTCACTGCCACCTGCGTGGCGCTTTCGTGG 414  
 QY 152 TGGGGGTGAGCGGCAACGTGTGACCGTGTGATCGGGCGTACCGGACATGCGGA 211  
 Db 415 TGGGCATCTCGGCAACCTGCTCACCATGCTGGTGTCCCGCTTCGCGAGCTGGCA 474  
 QY 212 CCACACCAACTTGTACCTGGGCGAGATGGCGGTGTCGACCTACTATCTCTGCTGGGC 271  
 Db 475 CCACACCAACCTTACCTATCCAGATGGCGCTTCGCGATGCTGCTATCTTCTGTGCA 534  
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 Db 535 TGGCGCTGACCTCTGCGCGCTCTCGCGATTCGCGCTTGGAACTTCGCGGACCTGCTCT 594  
 QY 332 GCGCGCTGTCTTACGTGGCGAGGCTGCACCTAGCCACGCTGTGACACATGACCG 391  
 Db 595 GCAACTCTTCAGTTTGTACGAGAGAGCTGCACCTAGCCACGCTTCTCACCATCAG 654  
 QY 392 CGCTCAGCGTTCAGCGCTTACGTGGCATCTGCGCGCGCTTCGCGCGCGCTGCTCTGCGG 451  
 Db 655 CGCTCAGCGTTCAGCGCTTACGTGGCATCTGCGCGCGCTTCGCGCGCGCTGCTCTGCGG 714  
 QY 452 CCCGCGCGCGTTCGCGCGCTTACGTGGCATCTGCGCGCGCTTCGCGCGCGCTGCTCTGCGG 511  
 Db 715 CCAAGGCGCGTGTGAAGCTGTGCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 774  
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 Db 775 GCGCCATCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 816

RESULT 3  
 C0959476  
 LOCUS AGENCOURT\_30842629 NIH\_MGC\_146 Homo sapiens cDNA clone  
 IMAGE:7389798 5', mRNA sequence.

C0959476  
 C0959476  
 EST.  
 Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 688)  
 NIH-MGC <http://mgi.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: Guthrie cDNA Resource Center  
 cDNA Library Preparation: Guthrie cDNA Resource Center  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: IRB18 row: c column: 04  
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 Location/Qualifiers

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from commercially available cDNA libraries) and cloned by  
 the Guthrie cDNA Resource Center ([www.guthrie.org/cDNA](http://www.guthrie.org/cDNA))  
 into pcDNA3.1. For specific information on cloning sites  
 (which vary by clone), please refer to the Guthrie  
 website, using the Guthrie ID given in the file  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBF.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBF.presv.dat)  
 a. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 18.4%; Score 228.4; DB 7; Length 688;  
 Best Local Similarity 79.8%; Pred. No. 8.e-39;  
 Matches 265; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
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 Db 3 ATGGGCGACCCCTGGAACGAGCGACGCGCCCCGAGGGGGCGGAGCGCCCGTGGCCC 62  
 QY 61 GCGGTGCGCGCTTCGCGAGCGCGCTGCTGCGCTTTCCTTCCCTGGGGCGCTGCTGGCG 120  
 Db 63 GCGGTGCGCGCTTCGCGAGCGCGCTGCTGCGCTTTCCTTCCCTGGGGCGCTGCTGGCG 122  
 QY 121 GTGACCGCTGTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
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 Db 183 TTGTTGCTCTGGCGCTGTGCGGNGTGTGGGGCTCTTCTCTCTTGGCCCTTGGGGCGCGCG 242  
 QY 241 GCGGTGCGGACCTACTCATCTGCTGCGGCTGCGCTTTCGACCTGACCGCTCTGGCGCG 300  
 Db 243 TGGGTGCTCTGNNGTCTCTCCCGGTTGNGCGNGGTGGCGGTGTTTCGGCCCTTGGCTC 302  
 QY 301 TCGCGCGCTCGGTGTTTCGGGCGCTGCTCTG 332  
 Db 303 TCGTGGGCTGTTGTTCCCGGTGTGCTTGG 334

## RESULT 4

C0959476  
 LOCUS CD618070/c 640 bp mRNA linear EST 12-JAN-2004  
 DEFINITION 56030361H1 FLP Homo sapiens cDNA, mRNA sequence.

C0959476  
 C0959476  
 EST.  
 Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 640)  
 Fu.G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)

JOURNAL  
 COMMENT  
 Contact: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: [gfu@incyte.com](mailto:gfu@incyte.com)

Location/Qualifiers  
 1..640  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

## FEATURES

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 Query Match 18.4%; Score 227.8; DB 6; Length 640;  
 Best Local Similarity 68.3%; Pred. No. 1.2e-38;  
 Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;  
 QY 93 GCCCTTTCCCTGGGGCGCTGTTGCCGCTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 152

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481 GCTCTTCCCGCGCGTCTGTCGGCGCGTACAGCCACCTGCTGGCACTCTTCGTGT 422
153 CGGGGTAGCGGCAACGTTGACCGTGTATGTCGCGGCGCTACCGGAGACATCGGAC 212
421 GGGTATCGTGGCAACCTGCTCACCATGCTGGTGTGTCGCGCTTCCGCGAGCTCGCAC 362
213 CACCAACCACTGTACCTGGGAGAGATGCGCGTGTCCGACCTACTCATCTGCTGGGT 272
361 CACCAACCACTGTACCTGGGAGAGATGCGCGTGTCCGACCTACTCATCTGCTGGGT 302
273 GCGGTTGCACTGTACCGGCTCTGGCGCTCGCGGCGCTGGGTGTTCGGGCGGCTCTGTG 332
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333 GCGGTTGCACTGTACCGGCTCTGGCGCTCGCGGCGCTGGGTGTTCGGGCGGCTCTGTG 392
241 CAAACTCTTCCAAATTCGTGAGTGTGAGAGTGTGACCTACGCGAGTGTGACCATCACAGC 182
393 GCTCAGCGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 452
181 GCTGAGCGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 122
453 CCGGCGCGCGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 512
121 CAAAGGGCGGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 62
513 TCCCTTCTTGTTCCTGTTGGGCGTGTGAGCGCGTGTGCGGCGCGTGTGCGGCGCGTGTGTCAC 555
61 GCCCATCTTCTGCTGTGAGTGTGAGCGCGTGTGAGCGCGTGTGCGGCGCGTGTGTCAC 19

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RESULT 5
CD618071
LOCUS 56030361J1 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
ACCESSION CD618071
VERSION CD618071.1 GI:40266336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS Fu G.K., Wang J.T., Yang J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

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FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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ORIGIN
Query Match 18.4%; Score 227.8; DB 6; Length 640;
Best Local Similarity 68.3%; Pred. No. 1.2e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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93 GCCCTTTCCCTTGGGGCGCTGTCGCGGTGACCGGTGTGTCCTGTGCTGTGCTGTGCTGT 152
157 GCTCTTCCCGCGCGCTGTCGCGGCGTGTGACCGGTGTGTCCTGTGCTGTGCTGTGCTGT 216
153 CCGGTTGAGCGGACGTTGTCACCGTGTGTCGCGGCGTGTGTCCTGTGCTGTGCTGTGCTGT 212
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213 CACCACCAACTTGTACCTGGGAGAGATGCGCGTGTCCGACCTACTCATCTGCTGTGCGGT 272
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273 GCGGTTGCACTGTACCGGCTCTGGCGCTCGCGGCGCTGGGTGTTCGGGCGGCTGTGCTGTG 332
337 GCGGTTGCACTGTACCGGCTCTGGCGCTCGCGGCGCTGGGTGTTCGGGCGGCTGTGCTGTG 396
333 GCGGTTGCACTGTACCGGCTCTGGCGCTCGCGGCGCTGGGTGTTCGGGCGGCTGTGCTGTG 392
397 CAAACTCTTCCAAATTCGTGAGTGTGAGAGTGTGACCTACGCGAGTGTGACCATCACAGC 456
393 GCTCAGCGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 452
457 GCTGAGCGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 516
453 CCGGCGCGCGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 512
517 CAAAGGGCGGTGTGAGCGCTACCTGCGCATCTGCGGCGCGTGTGCGGCGCGCTGTGTCAC 576
513 TCCCTTCTTGTTCCTGTTGGGCGTGTGAGCGCGTGTGCGGCGCGTGTGCGGCGCGTGTGTCAC 555
577 GCCCATCTTCTGCTGTGAGTGTGAGCGCGTGTGAGCGCGTGTGCGGCGCGTGTGTCAC 619

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RESULT 6
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LOCUS Homo sapiens GHR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407664
VERSION AY407664.1 GI:39763635
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 68.3%; Pred. No. 1.2e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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93 GCCCTTTCCCTTGGGGCGCTGTCGCGGTGACCGGTGTGTCCTGTGCTGTGCTGTGCTGT 152

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/clone_lib="MARC 3B0V"
/note=vector: pcwv SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

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279	GCAAACTCTTCCAGTTTGTACAGAGAGCTGCACCTACGCTACGGTGCTCACCATCACCG	338
Db		
392	CGCTCAGCGTGCAGCGCTACTGGCCATCTGCCGCCCGCTCCGCGCCCGCTCTTGGTCA	451
Qy		
339	CGCTCAGCGTGCAGCGCTACTTCCCATCTGCTTCCCGCTCGGGCCCAAGTGGTGATCA	398
Db		
452	CCGCGCGCGCGTCCGCGCGCTCATCGCTGTGCTCTGGGCGCTGGCGGCTCTCTCTGCCG	511
Qy		
399	CCAAGGCGGGTGAAGCTCGATCTCTGGTTCATCTGGGCCCTGGCTTCTCTGACGCGCG	458
Db		
512	GTCCCTCTTTGTCTCTGTGGCGGCTCGACGACGACCCCGCGCA	553
Qy		
459	GGCCCATCTTCGTGCTGTGTCCGAGTGGAGCATGAGAAATGCA	500
Db		

339	CGCTGAGCGT	CGAGCGCT	TACTTGGCCAT	TGTTCCCGCT	CGGGGCAAGG	TGGTGATCA	398
Db							
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QY							
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Db							
512	GTCCCTCT	TCTTTCTTC	TCTGGTGGGCG	TCGAGCAGG	ACCCCGCA		553
QY							
459	GGCCCATCT	TCTGTCGTGT	CGAGTGGG	GAGCATGAG	AATGCA		500
Db							

Qy	512	GTCCCTTCTTGTTCCTGCTGGCGCTCGAGCAGGACCCCGGCA	553
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CD618076/c	CD618076	637 bp	mRNA	linear
LOCUS	56030461H1	F1P Homo sapiens	cDNA	mRNA sequence.
DEFINITION				

EST 12-JAN-2000

**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 337)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK

**FEATURES**

**source**

1. 637

Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: giv@incyte.com.

Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="PLP"



FLC I."

ORIGIN	Query Match	17.7%	Score 219.2	DB 6	Length 608
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Db	2	TGGCGCTCTTCGTGGTGGGCATCTCGGGCAACCTGCTCACCATGCTGGTGGTGTCCCGCT	61		
Qy	197	ACGGGACATGCGGCAGCACCAACCTTGTAACCTGGGCAGCATGGCCCGTGTCCGACCTAC	256		
Db	62	TCCGCGAGCTGGCAGCACCAACCACTTACCTATCCAGCATGSCCTTCTCCGATCTGC	121		
Qy	257	TCATCTGCTCGGGCTGCGGTTGCACCTGTACCGGCTCTGGCGCTCGGGGCGCTGGGTGT	316		
Db	122	TCATCTTCTCTGTGATCCGCTGGACCTCGTCCGCGCTCTGGCAGTATCGGGCGCTGGAACT	181		
Qy	317	TCGGGCGCGTGTCTGCGCGCTGTCCCTCTACGTGGGCGGGGCTGCACCTACGCCACGC	376		
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Qy	437	CCGCGGCTTTGGTCAACCGCGCGCGCTGCGCGCGCTCATCGCTGTGCTCTGGGCGCGTGG	496		
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Qy	497	CGTGTCTCTGCGGTCCTTCTTGTTCGTGGGCGTTCGACGAGCAACCCCGCA	553		
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LOCUS	Pan troglodytes GHSR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION	AY407665				
ACCESSION	AY407665.1	GI:39763636			
VERSION					
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 969)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 969)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
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gene					

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/gene="GHSR"  
/locus tag="HCM2966"
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[illegible]





**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLC2778 row: p column: 05  
High quality sequence stop: 534.

**FEATURES**  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6577973"  
/tissue="IMAGE:teratocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC\_109"  
/note="Organ: ovary; Vector: pOTB7; Site: 1: ECORI; Site 2:  
XhoI; cDNA made by oligo-dT priming. directionally cloned  
into ECORI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

**ORIGIN**  
Query Match 15.0%; Score 186.4; DB 5; Length 843;  
Best Local Similarity 91.0%; Pred. No. 1e-29;  
Matches 243; Conservative 0; Mismatches 17; Indels 7; Gaps 4;  
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DB 534 GGTGGTCTTGCCATTATTAATTTGGTGTGGCTTCCAGTGGCAGAAATCAATTTACAT 593  
QY 966 AACACGGAGATTCGGGATGATGTACTTCTCTCAGTACTTTAAACATCGTCGCTCTGCA 1025  
DB 594 AACACGGAGATTCGGGATGATGTACTTCTCTCAGTACTTTAAACATCGTCGCTCTGCA 653  
QY 1026 ACTTTTCTATCTGAGGGCATCTATCAACCAATCTCTCAACCTC-ATTTCAAAGAAGT 1084  
DB 654 ACTTTTCTATCTGAGGGCATCTATCAACCAATCTCTCAACCTCAATTTCAAGAGT 713  
QY 1085 AC-AGAGCGCGCGCTTTAAA-----CTGCTGTGCGAAGGAAGTCCAGCGCGAG-AGGCT 1138  
DB 714 ACAAGAGCGCGCGCTTTAAACTGTCTGTTCGAGGGAAGTCCCAGCGCGAAGGCT 773  
QY 1139 TCCACAGACGAGGACACTGCGGGG 1165  
DB 774 CCCACAGACGAGGACACTGCGGGG 800

**RESULT 15**  
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LOCUS 56030445J1 FLP Homo sapiens cDNA, mRNA sequence.  
DEFINITION CD618075  
ACCESSION CD618075.1 GI:40266340  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 635)  
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)

**AUTHORS**  
**TITLE**  
**JOURNAL**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2005, 12:58:01 ; Search time 68.6667 Seconds  
(without alignments)  
2320.562 Million cell updates/sec

Title: US-09-719-485-3

Perfect score: 2155

Sequence: 1 MGSPWNGSDGPEGAREPWP.....DTGDTGVGYTETSANVTMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2155	100.0	412	3	AA54145 Amino aci
2	2155	100.0	412	4	AAB68478 Amino aci
3	2155	100.0	412	4	AAB62652 Long form
4	2155	100.0	412	5	ABG30936 Human G p
5	2155	100.0	412	6	ABP81993 Human mot
6	2155	100.0	412	8	ADN11761 Human mot
7	2155	100.0	412	8	ADQ29697 Human GPC
8	2155	100.0	412	8	ADQ37921 Human G-p
9	2155	100.0	501	4	AAG65822 Human GPR
10	2149	99.7	412	3	AAB02854 Human G p
11	2149	99.7	412	8	ADG86491 Human hGP
12	2149	99.7	412	8	ADG86511 Human orp
13	2149	99.7	412	8	ADP20284 Human GPC
14	2141	99.4	412	5	ABB09535 Human mot
15	2141	99.4	412	8	ADN12079 Protein #
16	1747	81.1	400	4	AAB68477 Amino aci
17	1581	73.4	386	3	AA54146 Amino aci
18	1581	73.4	386	4	AAB62653 Short for
19	1581	73.4	386	8	ADN11763 Human mot
20	1149.5	53.3	271	4	AAB68476 Amino aci
21	907	42.1	363	3	AA54147 The puffe
22	907	42.1	363	4	AAB68479 Amino aci
23	865.5	40.2	349	3	AA54147 A canine
24	863.5	40.1	366	3	AA54145 Human G p
25	863.5	40.1	366	3	AA54145 Human G p

26	863.5	40.1	366	4	AAB97376 Rat growt
27	863.5	40.1	366	4	AAB62650 Human G-p
28	863.5	40.1	366	5	AB09534 Human ghr
29	863.5	40.1	366	7	ADC22607 Human G p
30	863.5	40.1	366	7	ADH14080 Human GHS
31	863.5	40.1	366	8	ADD35398 Human gro
32	863.5	40.1	366	8	ADN12078 Protein #
33	863.5	40.1	366	8	ADN11756 Human gro
34	863.5	40.1	366	8	ADO29025 Human nov
35	863.5	40.1	366	8	ADQ28857 Human ghr
36	863	40.0	353	2	AAW19215 Swine gro
37	863	40.0	353	2	AAW19608 Pig growt
38	861.5	40.0	364	3	AA54565 A mouse g
39	861.5	40.0	364	4	AAB97377 Rat growt
40	861.5	40.0	364	8	ADO29026 Mouse nov
41	860	39.9	361	2	AAW19217 Human gro
42	860	39.9	362	2	AAW19610 Human gro
43	857.5	39.8	364	2	AAW19613 Rat growt
44	857.5	39.8	366	3	AA54145 Human mut
45	857.5	39.8	366	7	ADC22729 Human G p

#### ALIGNMENTS

RESULT 1  
AA54145  
ID AA54145 standard; protein; 412 AA.

XX AA54145;

AC AA54145;

DT 27-MAR-2000 (first entry)

XX Amino acid sequence of the motilin receptor splice variant MTL-R1A.

XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;

KW spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;

KW functional defect; neurological disorder; scleroderma; colonoscopy;

KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;

KW infection; stress-related motility disorder; psychogenic disorder;

KW gastroparesis; gastro-oesophageal reflux disease; constipation;

KW chronic idiopathic pseudo obstruction; acute faecal impaction;

KW postoperative ileus; gallstones; infantile colic; diarrhoea;

KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;

KW endoscopy; duodenal intubation.

XX Homo sapiens.

XX WO9964436-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012773.

XX 12-JUN-1998; 98US-0089098P.

XX (MERI ) MERCK & CO INC.

XX Feighner SD, Patchett AA, Tan C, Mckee K, Macneil D, Howard AD;

XX Pong S, Smith RG;

XX WPI; 2000-105868/09.

XX N-PSDB; AA45403.

XX Novel receptor protein for screening compounds used in treating irritable

XX bowel syndrome, constipation and other gastric conditions.

XX Claim 3; Fig 3; 44pp; English.

XX The present sequence represents splice variant MTL-R1A of the motilin

XX receptor. The gene encodes a G-protein coupled receptor, and is

XX designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A

XX (see AA54145) and MTL-R1B (see AA54146). MTL-R1A is a functional seven

transmembrane domain form, and MTL-RIB is a truncated five transmembrane domain. The MTL-R1 proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological disorders e.g. scleroderma, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychogenic disorders, gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathic pseudo obstruction, acute faecal impaction, postoperative ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy, endoscopy and duodenal intubation

XX Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 3; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;  
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60  
 DB 1 MGSPWNGSDGPGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60

QY 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120  
 DB 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120

QY 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180  
 DB 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180

QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPETAEEAALFSRECRPSPA 240  
 DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPETAEEAALFSRECRPSPA 240

QY 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHQTAVRL 300  
 DB 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHQTAVRL 300

QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
 DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360

QY 361 KYRAAAFKLLARKSRPRGFHRSRTAGEVAGDTGGDTVGYTETSANVKTWG 412  
 DB 361 KYRAAAFKLLARKSRPRGFHRSRTAGEVAGDTGGDTVGYTETSANVKTWG 412

# RESULT 2

AAAB68478  
 ID AAB68478 standard; protein; 412 AA.

AC AAB68478;

DT 23-JUL-2001 (first entry)

XX Amino acid sequence of a human motilin receptor polypeptide.

XX Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW Gastroparesis; irritable bowel syndrome; diarrhoea.

XX Homo sapiens.

PN WO200132710-A1.

XX 10-MAY-2001.

XX 25-OCT-2000; 2000WO-US029426.

XX 29-OCT-1999; 99US-0162264P.

XX (MERI) MERCK & CO INC.

XX Tan C, McKee K;

XX WPI; 2001-343479/36.  
 DR N-P8DB; AAF85449.  
 XX Novel polypeptides related to dog and rabbit motilin receptor  
 PT polypeptide, comprising unique regions from dog and motilin receptor  
 PT amino acid sequence, useful for identifying compounds for treating  
 PT diarrhea in humans.  
 XX Disclosure; Page 32-33; 42pp; English.  
 PS The present sequence represents a human motilin receptor polypeptide. The  
 CC specification describes a unique sequence present in exon 1 of the dog  
 CC motilin receptor, which is not present in human or Sphaeroides naphelus  
 CC 7587 motilin receptor sequences. The unique nucleic acid sequence is  
 CC useful for measuring the ability of a compound to affect motilin receptor  
 CC activity. Motilin receptor polynucleotides and polypeptides are used to  
 CC identify therapeutic compounds which are useful for treating  
 CC gastrointestinal diseases and disorders such as gastric motility  
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea  
 XX Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 4; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;  
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60  
 DB 1 MGSPWNGSDGPGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60

QY 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120  
 DB 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120

QY 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180  
 DB 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180

QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPETAEEAALFSRECRPSPA 240  
 DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPETAEEAALFSRECRPSPA 240

QY 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHQTAVRL 300  
 DB 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHQTAVRL 300

QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
 DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360

QY 361 KYRAAAFKLLARKSRPRGFHRSRTAGEVAGDTGGDTVGYTETSANVKTWG 412  
 DB 361 KYRAAAFKLLARKSRPRGFHRSRTAGEVAGDTGGDTVGYTETSANVKTWG 412

# RESULT 3

AAAB62652  
 ID AAB62652 standard; protein; 412 AA.

XX AAB62652;

XX 23-JUL-2001 (first entry)

XX Long form of motilin receptor, GPR-38A isoform.

XX zsig33; signal transduction; hormone; enzyme; neural development;  
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;  
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;  
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.

XX Homo sapiens.



XX SQ Sequence 412 AA;  
Query Match 100.0%; Score 2155; DB 5; Length 412;  
Best Local Similarity 100.0%; Pred. No. 3.8e-195;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFVVGVSGNVVTV 60  
DB 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFVVGVSGNVVTV 60  
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120  
DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120  
QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
DB 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
QY 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
DB 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRHRGTVRVL 300  
DB 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRHRGTVRVL 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFVLSINPILYNLSK 360  
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFVLSINPILYNLSK 360  
QY 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTETTSANVKTWG 412  
DB 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTETTSANVKTWG 412

RESULT 5  
ABP81993  
ID ABP81993 standard; protein; 412 AA.  
XX AC ABP81993;  
XX DT 04-MAR-2003 (first entry)  
XX DE Human motilin receptor GPR38 protein SEQ ID NO:473.  
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.  
XX OS Homo sapiens.  
XX PN WO200261087-A2.  
XX PD 08-AUG-2002.  
XX PF 19-DEC-2001; 2001WO-US050107.  
XX PR 19-DEC-2000; 2000US-0257144P.  
XX PP (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX PI Burner GC, Roush CL, Brown JP;  
XX DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42842.  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
XX autoimmune diseases.  
XX Disclosure; Fig 1; 523pp; English.  
XX The present invention describes antigenic peptides (1) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related diseases, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention  
XX SQ Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 6; Length 412;  
Best Local Similarity 100.0%; Pred. No. 3.8e-195;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFVVGVSGNVVTV 60  
DB 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFVVGVSGNVVTV 60  
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120  
DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120  
QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
DB 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
QY 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
DB 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRHRGTVRVL 300  
DB 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRHRGTVRVL 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFVLSINPILYNLSK 360  
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFVLSINPILYNLSK 360  
QY 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTETTSANVKTWG 412  
DB 361 KYRAAFAKLLARKSRPRGHRSDTAGVAGDTGGDTGVGTETTSANVKTWG 412

RESULT 6  
ADN11761  
ID ADN11761 standard; protein; 412 AA.

XX AC ADN11761;  
 XX DT 15-JUL-2004 (first entry)  
 XX DE Human motilin receptor GPR-38A protein.  
 XX KW human; zsig33; body weight; body mass; antibody; antagonist;  
 KW gastrointestinal; antiinflammatory; antitumor; antitumor;  
 KW growth hormone secretagogue; GHS-R; peptide-antibody complex;  
 KW motilin receptor.  
 XX OS Homo sapiens.  
 XX PN WO2004033645-A2.  
 XX PD 22-APR-2004.  
 XX PF 06-OCT-2003; 2003WO-US031804.  
 XX PR 07-OCT-2002; 2002US-0416918P.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;  
 XX DR WPI; 2004-340913/31.  
 XX DR N-PSDB; ADN11760.  
 XX PS Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,  
 PT inhibiting signal transduction in a cell expressing a growth hormone  
 PT secretagogue receptor, or treating a metabolic disorder.  
 XX PS Disclosure; Page 95-96; 100pp; English.  
 XX CC The present invention relates to the use of a zsig33 peptide for forming  
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal  
 CC transduction in a cell expressing a growth hormone secretagogue receptor  
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite  
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a  
 CC mammal, or treating a metabolic disorder. The peptide is useful for  
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting  
 CC signal transduction in a cell expressing a GHS-R, decreasing fat  
 CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting  
 CC growth hormone secretion in pituitary cells of a mammal, or treating a  
 CC metabolic disorder. The zsig33 polypeptides can be used to study  
 CC proliferation or differentiation in stomach, lung, pituitary,  
 CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,  
 CC skeletal muscle or pancreas. They are also useful in delivering  
 CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are  
 CC also useful for promoting wound healing. The polypeptides, nucleic acids  
 CC and antibodies are useful for diagnosing, treating or preventing  
 CC disorders associated with gastric reflux, gastroparesis, modulation of  
 CC secretion of pituitary hormones, including growth hormone, Crohn's  
 CC disease, metabolic wasting, gastric ulcers, weight management, or  
 CC degenerative disease. The present sequence is the human motilin receptor  
 CC GPR38A protein shown in the exemplification of the invention.  
 XX SQ Sequence 412 AA;  
 Query Match 100.0%; Score 2155; DB 8; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;  
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGSPWNGSDGPGAGPPWALPPCDRCRSPFPLGALVPVAVCLCLFVGVSGNVTV 60  
 DB 1 MGSPWNGSDGPGAGPPWALPPCDRCRSPFPLGALVPVAVCLCLFVGVSGNVTV 60  
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSPWVFGPLLCRLSLYVGE 120  
 DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSPWVFGPLLCRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVRYLAICRPLRVLVTRRRVRLALIAVLWAVALLSAGPFLVLGVE 180

Db 121 CTYATLLHMTALSVRYLAICRPLRVLVTRRRVRLALIAVLWAVALLSAGPFLVLGVE 180  
 QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPPPETAATAAALFSRECRPSPA 240  
 Db 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPPPETAATAAALFSRECRPSPA 240  
 QY 241 QLGALRVMLWVTYAYFFLPFLCLSLYLGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
 Db 241 QLGALRVMLWVTYAYFFLPFLCLSLYLGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
 QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLSK 360  
 Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLSK 360  
 QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412  
 Db 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

RESULT 7  
 ADO29697  
 ID ADO29697 standard; protein; 412 AA.  
 AC ADO29697;  
 XX 29-JUL-2004 (first entry)  
 XX Human GPCR GPR38, SEQ ID NO:799.  
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 KW cytosolic; antinflammatory; vasotropic; antidiabetic; antidiabetic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiarrhoeic;  
 KW virucide; hepatotropic; antibacterial; antianemic; antiepileptic;  
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; receptor.  
 XX Homo sapiens.  
 OS WO2004040000-A2.  
 PN 13-MAY-2004.  
 PD 09-SEP-2003; 2003WO-US028226.  
 PF 09-SEP-2002; 2002US-0409303P.  
 PR 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRIMAL INC.  
 XX Gaitanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
 XX WPI; 2004-390329/36.  
 DR N-PSDB; ADO30072.  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX Claim 151; SEQ ID NO 799; 542pp; English.  
 PS The invention relates to human and mouse G protein-coupled receptors  
 XX CC

(GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

XX SQ Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 8; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;  
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLFVVGSGNVTV 60  
 DB 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLFVVGSGNVTV 60

QY 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120  
 DB 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180  
 DB 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180

QY 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAFAAALFSRECRPSA 240  
 DB 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAFAAALFSRECRPSA 240

QY 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300  
 DB 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300

QY 301 LVVLAFFICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLSK 360  
 DB 301 LVVLAFFICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLSK 360

QY 361 KYRAAFAKLLARKSRPGFHSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412  
 DB 361 KYRAAFAKLLARKSRPGFHSRDTAGEVAGDTGGDTGVGTETTSANVKTWG 412

RESULT 8

ADQ37921

ID ADQ37921 standard; protein; 412 AA.

XX ADQ37921;

AC ADQ37921;

XX 23-SEP-2004 (first entry)

XX DE Human G-protein-coupled receptor 38 protein.  
 XX KW antiparkinsonian; neuroprotective; nootropic; cardiovascular; cardiant;  
 KW vasotropic; antiarteriosclerotic; nephrotropic; uropathic;  
 KW urology disease; cardiovascular disease;  
 KW peripheral nervous system disorder; central nervous system disorder;  
 KW G-protein-coupled receptor 38; GPR38; Parkinson's disease;  
 KW multiple sclerosis; dementia; myocardial infarction; ischemic disease;  
 KW atherosclerosis; renal failure; glomerulopathy; urinary incontinence.  
 XX OS Homo sapiens.  
 XX PN WO2004057328-A2.  
 XX PD 08-JUL-2004.  
 XX PF 11-DEC-2003; 2003WO-EP014052.  
 XX PR 23-DEC-2002; 2002EP-00028753.  
 XX PA (FARB ) BAYER HEALTHCARE AG.  
 XX PI Goltz S, Brueggemeier U, Summer H;  
 XX WIPI: 2004-543310/52.  
 XX DR N-FSDB; ADQ37920.  
 XX PT Screening therapeutic agents for use in treatment of urology diseases and  
 PT cardiovascular diseases in a mammal, comprises contacting a test compound  
 PT with G-protein-coupled receptor 38, and detecting binding.  
 XX PS Disclosure; SEQ ID NO 2; 111pp; English.

CC The invention relates to a method of screening (M1) for therapeutic  
 CC agents useful in the treatment of a disease chosen from urology diseases,  
 CC cardiovascular diseases and disorders of the peripheral and central  
 CC nervous system in a mammal, comprises contacting a test compound with a G  
 CC -protein-coupled receptor 38 (GPR38) polypeptide, and detecting binding  
 CC of the test compound to the GPR38 polypeptide. (M1) is useful for  
 CC screening therapeutic agents useful in the treatment of a disease chosen  
 CC from urology diseases, cardiovascular diseases and disorders of the  
 CC peripheral and central nervous system in a mammal, such as Parkinson's  
 CC disease, multiple sclerosis, dementia, cardiovascular disorders such as  
 CC myocardial infarction, ischemic diseases, atherosclerosis, and urological  
 CC disorders such as acute or chronic renal failure, glomerulopathies, and  
 CC urinary incontinence. This sequence corresponds to the human G-protein-  
 CC coupled receptor 38.

XX SQ Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 8; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;  
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLFVVGSGNVTV 60  
 DB 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLFVVGSGNVTV 60

QY 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120  
 DB 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180  
 DB 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180

QY 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAFAAALFSRECRPSA 240  
 DB 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAFAAALFSRECRPSA 240

QY 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300  
 DB 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300



Db 241 QLGALRVMLWTTAYFFLPFLCLSLYLIGRELWSSRRPLRGPAASGRERHRTQTVRL 300  
Qy 301 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLVSASINPILYNLISK 360  
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLVSASINPILYNLISK 360  
Qy 361 KYRAAFAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412  
Db 361 KYRAAFAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

RESULT 9  
AAG65822  
ID AAG65822 standard; protein; 501 AA.  
XX  
AC AAG65822;  
XX  
DT 30-JAN-2002 (first entry)  
XX  
DE Human GPR38 variant GPR38V polypeptide.  
XX  
KW GPR38V; variant; antibacterial; cytostatic; analgesic; antiaesthetic;  
KW anti-Parkinsonian; hypotensive; antidiabetic; osteopathic;  
KW antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant;  
KW antiulcer; antiemetic; cardiant; vaccine; human.  
XX  
OS Homo sapiens.  
XX  
XX WO200164836-A2.  
XX  
XX PD 07-SEP-2001.  
XX  
XX PF 28-FEB-2001; 2001WO-US006277.  
XX  
XX PR 01-MAR-2000; 2000US-00516315.  
XX  
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX PI Elshourbagy N, Shabon U;  
XX  
XX DR WPI; 2001-638956/73.  
XX  
XX DR N-PSDB; AAI6989.  
XX  
XX PT New human GPR38V polypeptide and polynucleotide, useful for treating e.g.  
XX bacterial, fungal, protozoal and viral infections, cancers or allergies,  
XX as vaccines, and for identifying agonists and antagonists potentially  
XX useful in therapy.  
XX  
XX PS Claim 1; Page 26; 32pp; English.  
XX  
XX CC This represents a human GPR38 variant (GPR38V) polypeptide. GPR38V can be  
XX expressed by standard recombinant methodology. The polynucleotides and  
XX polypeptides are used in the treatment of bacterial, fungal, protozoal  
XX and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,  
XX diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart  
XX failure, hypertension, urinary retentions, osteoporosis, allergies,  
XX ulcers, migraine, psychotic and neurological disorders, or dyskinesias.  
XX They are also useful for identifying agonists and antagonists that are  
XX potentially useful in therapy, as vaccines to induce immunological  
XX response in a mammal. The polypeptides may also be used as immunogens to  
XX produce antibodies immunospecific for the polypeptides, and to identify  
XX membrane bound or soluble receptors

SQ Sequence 501 AA;  
Query Match 100.0%; Score 2155; DB 4; Length 501;  
Best Local Similarity 100.0%; Pred. No. 4.8e-195;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGSPWNGSGEGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFVVGSGNVVTV 60  
Db 90 MGSPWNGSGEGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFVVGSGNVVTV 149

Qy 61 MLICRYDMRTTNNLYLGSMVAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
Db 150 MLICRYDMRTTNNLYLGSMVAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 209  
Qy 121 CTYATLHMTALSVERYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180  
Db 210 CTYATLHMTALSVERYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFLVGVE 269  
Qy 181 QDPGISVVGINGLTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSPA 240  
Db 270 QDPGISVVGINGLTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSPA 329  
Qy 241 QLGALRVMLWTTAYFFLPFLCLSLYLIGRELWSSRRPLRGPAASGRERHRTQTVRL 300  
Db 330 QLGALRVMLWTTAYFFLPFLCLSLYLIGRELWSSRRPLRGPAASGRERHRTQTVRL 389  
Qy 301 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLVSASINPILYNLISK 360  
Db 390 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLVSASINPILYNLISK 449  
Qy 361 KYRAAFAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412  
Db 450 KYRAAFAFKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 501

RESULT 10  
AAB02854  
ID AAB02854 standard; protein; 412 AA.  
XX  
AC AAB02854;  
XX  
DT 22-AUG-2000 (first entry)  
XX  
DE Human G protein coupled receptor hGPR38 (V297K) protein SEQ ID NO:130.  
XX  
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO2000022131-A2.  
XX  
XX PD 20-APR-2000.  
XX  
XX PF 13-OCT-1999; 99WO-US024065.  
XX  
XX PR 13-OCT-1998; 98US-00170496.  
XX PR 12-NOV-1998; 98US-0108029P.  
XX PR 20-NOV-1998; 98US-0109213P.  
XX PR 27-NOV-1998; 98US-0110060P.  
XX PR 16-FEB-1999; 99US-0120416P.  
XX PR 26-FEB-1999; 99US-0121852P.  
XX PR 12-MAR-1999; 99US-0123944P.  
XX PR 12-MAR-1999; 99US-0123945P.  
XX PR 12-MAR-1999; 99US-0123946P.  
XX PR 12-MAR-1999; 99US-0123948P.  
XX PR 12-MAR-1999; 99US-0123949P.  
XX PR 12-MAR-1999; 99US-0123951P.  
XX PR 28-MAY-1999; 99US-0136436P.  
XX PR 28-MAY-1999; 99US-0136437P.  
XX PR 28-MAY-1999; 99US-0136439P.  
XX PR 28-MAY-1999; 99US-0137127P.  
XX PR 28-MAY-1999; 99US-0137131P.  
XX PR 28-MAY-1999; 99US-0137567P.  
XX PR 29-JUN-1999; 99US-0141448P.  
XX PR 27-AUG-1999; 99US-0151114P.  
XX PR 03-SEP-1999; 99US-0152524P.  
XX PR 29-SEP-1999; 99US-0156555P.  
XX PR 29-SEP-1999; 99US-0156633P.  
XX PR 29-SEP-1999; 99US-0156634P.  
XX PR 29-SEP-1999; 99US-0156653P.  
XX PR 01-OCT-1999; 99US-0157280P.

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PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157283P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX (AREN-) ARENA PHARM INC.
PA
XX
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI; 2000-317986/27.
DR N-PSDB; AAA46116.
XX
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX
XX Example 2; Page 169-169; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptors agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 412 AA;
SQ
Query Match 99.7%; Score 2149; DB 3; Length 412;
Best Local Similarity 99.8%; Pred. No. 1.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWPAIPCCDERRCSPFFLGALVPVTAVALCLFVVGSGNVTV 60
Db 1 MGSPWNGSDGPEGAREPPWPAIPCCDERRCSPFFLGALVPVTAVALCLFVVGSGNVTV 60
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPPWVFGPLCLSLIYVGE 120
Db 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPPWVFGPLCLSLIYVGE 120
QY 121 CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRLIAVMAVALLSAGPFLVGV 180
Db 121 CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRLIAVMAVALLSAGPFLVGV 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPSPSPGPTAAALFSRECRPSA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLRAPPSPSPGPTAAALFSRECRPSA 240
QY 241 QLGALRVMLVMTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGAASGRERHQTVRVL 300
Db 241 QLGALRVMLVMTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGAASGRERHQTVRVL 300
QY 301 LVVLAFTICMLPFHVGRIIYINTEDSRMTYFSQVFNIVALQLFYLASINPILYNLSK 360
Db 301 LVVLAFTICMLPFHVGRIIYINTEDSRMTYFSQVFNIVALQLFYLASINPILYNLSK 360
QY 361 KYRAAFAKLLARKSRPRGHRSDTAGEVAGDTGGDTVGTETTSANVKTNG 412
Db 361 KYRAAFAKLLARKSRPRGHRSDTAGEVAGDTGGDTVGTETTSANVKTNG 412

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RESULT 11
ADG86491
ID ADG86491 standard; protein; 412 AA.
XX
AC ADG86491;
XX
DT 11-MAR-2004 (first entry)
XX

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DE Human hGPR38 V297K mutant protein.

XX Human; receptor; mutein; endogenous orphan GPCR;  
KW G protein-coupled receptor; transmembrane domain 6; mutant.

XX Synthetic.

OS Homo sapiens.

XX US2003229216-A1.

XX 11-DEC-2003.

XX 16-APR-2003; 2003US-00417820.

XX 13-OCT-1998; 98US-00170496.

XX 12-NOV-1998; 98US-0108029P.

XX 20-NOV-1998; 98US-0109213P.

XX 27-NOV-1998; 98US-0110060P.

XX 16-FEB-1999; 99US-0120416P.

XX 26-FEB-1999; 99US-0121852P.

XX 12-MAR-1999; 99US-0123944P.

XX 12-MAR-1999; 99US-0123945P.

XX 12-MAR-1999; 99US-0123946P.

XX 12-MAR-1999; 99US-0123948P.

XX 12-MAR-1999; 99US-0123949P.

XX 12-MAR-1999; 99US-0123951P.

XX 28-MAY-1999; 99US-0136436P.

XX 28-MAY-1999; 99US-0136437P.

XX 28-MAY-1999; 99US-0136439P.

XX 28-MAY-1999; 99US-0136567P.

XX 28-MAY-1999; 99US-0137127P.

XX 28-MAY-1999; 99US-0137131P.

XX 29-JUN-1999; 99US-0141448P.

XX 27-AUG-1999; 99US-0151114P.

XX 03-SEP-1999; 99US-0152524P.

XX 29-SEP-1999; 99US-0156555P.

XX 29-SEP-1999; 99US-0156633P.

XX 29-SEP-1999; 99US-0156634P.

XX 29-SEP-1999; 99US-0156653P.

XX 01-OCT-1999; 99US-0157280P.

XX 01-OCT-1999; 99US-0157281P.

XX 01-OCT-1999; 99US-0157282P.

XX 01-OCT-1999; 99US-0157293P.

XX 01-OCT-1999; 99US-0157294P.

XX 12-OCT-1999; 99US-00416760.

(CHEN/) CHEN R.

(LIAW/) LIAW C W.

(LOWI/) LOWITZ K.

(CHAL/) CHALMERS D T.

(BEHA/) BEHAN D P.

Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;

WPI; 2004-052038/05.

N-PSDB; ADG86490.

New cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor, useful for identifying receptor, inverse or partial agonists having potential applicability as therapeutic agents.

Example 2; SEQ ID NO 130; 110pp; English.

The invention relates to a cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising HARE-3 (F313K), HARE-4 (V233K), HARE-5 (A240K), HGPCR14 (L257K), HGPCR27 (C283K), HARE-1 (E232K), HARE-2 (G285K), hPR1 (L239K), hG2A (K232A), hRUP3 (L224K), hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K), hCHN3 (S284K), hCHN6 (L352K), hCHN8 (N235K) or hH9 (F236K). Also included are a non-endogenous version of a human G protein-coupled receptor encoded by the cDNA, a plasmid comprising the vector and the cDNA and a host cell comprising the plasmid. The cDNA encodes a non-endogenous, constitutively

CC activated version of a human G protein-coupled AT1 receptor comprising  
CC the angiotensin II type 1 receptor hAT1(F239K), hAT1(N111A),  
CC hAT1(AT2K255IC3, a domain swap mutant) or hAT1(A243+). The mutation is of  
CC an amino acid 16 residues from the proline in transmembrane domain 6 and  
CC is usually to a lysine. The cDNA is useful for identifying candidate  
CC compounds as receptor agonists, inverse agonists or partial agonists  
CC having potential applicability as therapeutic agents. The present  
CC sequence represents a mutated human GPCR.

XX Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 8; Length 412;  
Best Local Similarity 99.8%; Pred. No. 1.4e-194;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFPALGALVPVAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFPALGALVPVAVCLCLFVVGSGNVTV 60  
Qy 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120  
Qy 121 CTYATLHMTALSVERYLAI CRPLARVLVTRRVRALIAVLWALLSAGPFLVGV 180  
Db 121 CTYATLHMTALSVERYLAI CRPLARVLVTRRVRALIAVLWALLSAGPFLVGV 180  
Qy 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPPSPSPETAEEAALFSRECRPSPA 240  
Db 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPPSPSPETAEEAALFSRECRPSPA 240  
Qy 241 QLGALRVMLVMTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTKRVL 300  
Db 241 QLGALRVMLVMTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTKRVL 300  
Qy 301 LVVLAFTICWLPFHVGRIIINTEDSRMYPFSQYFNIVALQLFYLSASINPILYNLSK 360  
Db 301 LVVLAFTICWLPFHVGRIIINTEDSRMYPFSQYFNIVALQLFYLSASINPILYNLSK 360  
Qy 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVGTSTANVKTWG 412  
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVGTSTANVKTWG 412

RESULT 12  
ADG86511  
ID ADG86511 standard; protein; 412 AA.  
XX ADG86511;  
XX ADG86511;  
XX 11-MAR-2004 (first entry)  
XX Human orphan GPCR-associated protein #2.  
XX Human; endogenous orphan GPCR; G protein-coupled receptor;  
KW transmembrane domain 6.  
XX Homo sapiens.  
XX US2003229216-A1.  
XX 11-DEC-2003.  
XX 16-APR-2003; 2003US-00417820.  
XX 13-OCT-1998; 98US-00170496.  
XX 12-NOV-1998; 98US-0108029P.  
XX 20-NOV-1998; 98US-0109213P.  
XX 27-NOV-1998; 98US-0110060P.  
XX 16-FEB-1999; 99US-0120416P.  
XX 26-FEB-1999; 99US-0121852P.  
XX 12-MAR-1999; 99US-0123944P.  
XX 12-MAR-1999; 99US-0123945P.

PR 12-MAR-1999; 99US-0123946P.  
PR 12-MAR-1999; 99US-0123948P.  
PR 12-MAR-1999; 99US-0123949P.  
PR 12-MAR-1999; 99US-0123951P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0136567P.  
PR 28-MAY-1999; 99US-0137113P.  
PR 28-MAY-1999; 99US-0137117P.  
PR 28-MAY-1999; 99US-0141448P.  
PR 27-AUG-1999; 99US-0151114P.  
PR 03-SEP-1999; 99US-0152524P.  
PR 29-SEP-1999; 99US-0156555P.  
PR 29-SEP-1999; 99US-0156634P.  
PR 29-SEP-1999; 99US-0156653P.  
PR 01-OCT-1999; 99US-0157280P.  
PR 01-OCT-1999; 99US-0157281P.  
PR 01-OCT-1999; 99US-0157282P.  
PR 01-OCT-1999; 99US-0157293P.  
PR 01-OCT-1999; 99US-0157294P.  
PR 12-OCT-1999; 99US-00416760.  
XX (CHEN/) CHEN R.  
PA (LIAW/) LIAW C W.  
PA (LOWI/) LOWITZ K.  
PA (CHAL/) CHALMERS D T.  
XX (BEHA/) BEHAN D P.

PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;  
XX WPI; 2004-052038/05.  
XX New cDNA encoding a non-endogenous, constitutively activated version of a  
PT human G protein-coupled receptor, useful for identifying receptor,  
PT inverse or partial agonists having potential applicability as therapeutic  
PT agents.

Dislosure; SEQ ID NO 150; 110pp; English.

CC The invention relates to a cDNA encoding a non-endogenous, constitutively  
CC activated version of a human G protein-coupled receptor comprising HARE-  
CC 3(F313K), HARE-4(V233K), HARE-5(A240K), HGPCR14(L257K), HGPCR27(C283K),  
CC HARE-1(E232K), HARE-2(G285K), hPRP1 (L239K), hG2A(K232A), hRUP3(L224K),  
CC hRUP5(A236K), hRUP6(N267K), hRUP7(A302K), hCHN4(V236K), hMC4(V244K),  
CC hCHN3(S284K), hCHN6(L352K), hCHN8(N235K) or hH9(F236K). Also included are  
CC a non-endogenous version of a human G protein-coupled receptor encoded by  
CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell  
CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively  
CC activated version of a human G protein-coupled AT1 receptor comprising  
CC the angiotensin II type 1 receptor hAT1(F239K), hAT1(N111A),  
CC hAT1(AT2K255IC3, a domain swap mutant) or hAT1(A243+). The mutation is of  
CC an amino acid 16 residues from the proline in transmembrane domain 6 and  
CC is usually to a lysine. The cDNA is useful for identifying candidate  
CC compounds as receptor agonists, inverse agonists or partial agonists  
CC having potential applicability as therapeutic agents. The present  
CC sequence is a GPCR-associated protein included in the sequence listing  
CC but not mentioned anywhere else in the specification.

XX Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 8; Length 412;  
Best Local Similarity 99.8%; Pred. No. 1.4e-194;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFPALGALVPVAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFPALGALVPVAVCLCLFVVGSGNVTV 60  
Qy 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVRYLAICRPLRAVLTTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
Db 121 CTYATLLHMTALSVRYLAICRPLRAVLTTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
QY 241 QLGALRVMLWVTYAYFPLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300  
Db 241 QLGALRVMLWVTYAYFPLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300  
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVYFQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVYFQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGDTGVGYTETSANVKTMG 412  
Db 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGDTGVGYTETSANVKTMG 412

RESULT 13  
ADP20284  
ID ADP20284 standard; protein; 412 AA.  
XX  
AC ADP20284;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Human GPCR GPR38 V297K mutant.  
XX  
KW antiinflammatory; GPCR-agonist; GPCR-antagonist;  
KW G protein-coupled receptor; GPCR; GPCR modulator; inflammation;  
KW pharmaceutical composition; inflammatory disorder; human; hGPR38; mutant;  
KW mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US2004110238-A1.  
PD 10-JUN-2004.  
XX  
PF 26-NOV-2003; 2003US-00723955.  
XX  
PR 13-OCT-1998; 98US-00170496.  
PR 12-NOV-1998; 98US-0108029P.  
PR 20-NOV-1998; 98US-0109213P.  
PR 27-NOV-1998; 98US-0110060P.  
PR 16-FEB-1999; 99US-0120416P.  
PR 26-FEB-1999; 99US-0121852P.  
PR 12-MAR-1999; 99US-0123944P.  
PR 12-MAR-1999; 99US-0123946P.  
PR 12-MAR-1999; 99US-0123948P.  
PR 12-MAR-1999; 99US-0123949P.  
PR 12-MAR-1999; 99US-0123951P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0136567P.  
PR 28-MAY-1999; 99US-0137127P.  
PR 28-MAY-1999; 99US-0137131P.  
PR 29-JUN-1999; 99US-0141448P.  
PR 27-AUG-1999; 99US-0151114P.  
PR 03-SEP-1999; 99US-0152524P.  
PR 29-SEP-1999; 99US-0156555P.  
PR 29-SEP-1999; 99US-0156633P.  
PR 29-SEP-1999; 99US-0156634P.  
PR 29-SEP-1999; 99US-0156653P.  
PR 01-OCT-1999; 99US-0157280P.  
PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.  
PR 01-OCT-1999; 99US-0157293P.  
PR 01-OCT-1999; 99US-0157294P.  
PR 12-OCT-1999; 99US-00416760.  
PR 16-APR-2003; 2003US-00417820.  
XX (CHEN/) CHEN R.  
PA (LIAM/) LIAM C W.  
PA (LOWI/) LOWITZ K.  
PA (CHAL/) CHALMERS D T.  
PA (BEHA/) BEHAN D P.  
XX  
PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;  
XX WPI; 2004-440359/41.  
DR N-PSDB; ADP20283.  
XX  
PT Identifying one or more candidate compounds as a modulator of a G protein  
PT coupled receptor (GPCR), useful for treating disorders or conditions  
PT associated with expression or activity of the GPCR.  
XX  
PS Example 2; SEQ ID NO 130; 106pp; English.  
XX  
CC The invention describes a method of identifying one or more candidate  
CC compounds as a modulator of a G protein-coupled receptor that comprises a  
CC fully defined sequence of 337 amino acids (SEQ ID NO: 82), comprising  
CC contacting the one or more compounds with a host cell or with a membrane  
CC of a host cell that expresses the receptor, and measuring the ability of  
CC the compound or compounds to inhibit or stimulate functionality of the  
CC receptor. Also described are: a method for identifying one or more  
CC candidate compounds as a modulator of inflammation; a method for  
CC identifying one or more candidate compounds as a modulator of a G protein  
CC coupled receptor; a compound identified by any of the methods cited  
CC above; a pharmaceutical composition; a method of modulating the activity  
CC of a G protein-coupled receptor having the amino acid sequence of SEQ ID  
CC NO:82; a method of modulating inflammation in a mammal in need of the  
CC modulating; a method of inhibiting inflammation in a mammal in need of  
CC the inhibiting; a method of preventing or treating an inflammatory  
CC disorder in a mammal in need of the preventing or treating; and a method  
CC of treating an inflammatory disorder. The methods and compositions of the  
CC present invention are useful for the treatment of diseases or conditions  
CC associated with aberrant expression or activity of the GPCR e.g.  
CC inflammation. This is the amino acid sequence of human G protein coupled  
CC receptor (GPCR) hGPR38 V297K mutant.  
XX  
SQ Sequence 412 AA;  
Query Match 99.7%; Score 2149; DB 8; Length 412;  
Best Local Similarity 99.8%; Pred. No. 1.4e-194;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPHPALPPCDERRCSPFPGALVPTAVCLCLFWGVGNGVTV 60  
Db 1 MGSPWNGSDGPEGAREPPHPALPPCDERRCSPFPGALVPTAVCLCLFWGVGNGVTV 60  
QY 61 MLIGRYRDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPCLCLSLYVGG 120  
Db 61 MLIGRYRDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPCLCLSLYVGG 120  
QY 121 CTYATLLHMTALSVRYLAICRPLRAVLTTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
Db 121 CTYATLLHMTALSVRYLAICRPLRAVLTTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
QY 241 QLGALRVMLWVTYAYFPLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300  
Db 241 QLGALRVMLWVTYAYFPLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300  
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVYFQYFNIVALQLFYLSASINPILYNLISK 360

Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLASINPILYNLISK 360  
 QY 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412  
 Db 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412

RESULT 14  
 ID ABB09535  
 XX ABB09535 standard; protein; 412 AA.  
 AC ABB09535;  
 XX  
 DT 22-OCT-2002 (first entry)  
 DE Human motilin receptor.  
 XX  
 KW Human; motilin receptor; appetite; food intake; agonist; analogue;  
 KW undernutrition; anorexia; cachexia; malignant disease; infection;  
 KW inflammatory disease; weight loss; antagonist; obesity; anorectic;  
 KW anabolic; ghrelin receptor homologue; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200260472-A1.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 31-JAN-2002; 2002WO-JP000765.  
 XX  
 PR 31-JAN-2001; 2001JP-00024423.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Inui A, Asakawa A, Kaga T;  
 XX  
 DR WPI; 2002-619206/66.  
 XX  
 PT Remedies for diseases with hypo-nutrition status e.g. inappetence and  
 PT cachexia, containing ghrelin or its analogs including agonists and  
 PT antagonists.  
 XX  
 PS Disclosure; Fig 1B; 50pp; Japanese.  
 XX  
 CC The invention relates to the use of ghrelin or its analogues for the  
 CC treatment of diseases associated with undernutrition such as anorexia,  
 CC and also relates to the use of ghrelin antagonists for the prevention or  
 CC treatment of obesity. The invention additionally discloses a method for  
 CC screening ghrelin agonists or antagonists by measuring the amount of food  
 CC intake, neuropeptide Y (NPY) expression, binding of NPY to NPY receptor  
 CC Y1, oxygen consumption, gastric emptying, or activity of the vagus nerve.  
 CC Intracerebroventricular (ICV) administration of ghrelin in animals was  
 CC found to increase food intake over a period of 24 hours. Ghrelin and its  
 CC analogues may therefore be used to treat conditions such as loss of  
 CC appetite, anorexia, cachexia, malignant diseases, and weight loss  
 CC associated with infection or inflammatory diseases. Conversely, ghrelin  
 CC antagonists may be used in the treatment of obesity. The present sequence  
 CC represents the human motilin receptor, a homologue of the ghrelin  
 CC receptor (ABB09534) which is referred to in the disclosure of the  
 CC invention

Query Match 99.4%; Score 2141; DB 5; Length 412;  
 Best Local Similarity 99.5%; Pred. No. 8e-194;  
 Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFFLGALVPVTVAVCLCLFVVGSGNVTV 60  
 Db 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFFLGALVPVTVAVCLCLFVVGSGNVTV 60  
 QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120

Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120  
 QY 121 CTYATLLHMTALSVERVLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180  
 Db 121 CTYATLLHMTALSVERVLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180  
 QY 181 QDPGISVVPGLNGTARTIASSPPLWLSRAPPPSPGPETAAALFSRECRPSPA 240  
 Db 181 QDPGISVVPGLNGTARTIASSPPLWLSRAPPPSPGPETAAALFSRECRPSPA 240  
 QY 241 QLGALRVMLWVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRGRTVRL 300  
 Db 241 QLGALRVMLWVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRGRTVRL 300  
 QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLASINPILYNLISK 360  
 Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFYQYFNIVALQLFYLASINPILYNLISK 360  
 QY 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412  
 Db 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412

RESULT 15  
 ID ADN12079 standard; protein; 412 AA.  
 XX  
 AC ADN12079;  
 XX  
 DT 17-JUN-2004 (first entry)  
 DE  
 XX  
 KW Protein #4 associated with growth hormone secretagogue receptor.  
 KW diabetes; growth hormone secretagogue receptor; GHS-R; Antidiabetic;  
 KW Anorectic; obesity; blood sugar level; appetite.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004004772-A1.  
 XX  
 PD 15-JAN-2004.  
 XX  
 PF 03-JUL-2003; 2003WO-JP008482.  
 XX  
 PR 05-JUL-2002; 2002JP-00197582.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Inui A, Asakawa A;  
 XX  
 DR WPI; 2004-099347/10.  
 XX  
 PT Growth hormone secretagogue receptor antagonist for treatment of  
 PT diabetes, obesity and appetite control.  
 XX  
 PS Disclosure; SEQ ID NO 4; 44pp; Japanese.  
 XX  
 CC The present invention relates to a treatment and preventative agent for  
 CC diabetes comprises growth hormone secretagogue receptor (GHS-R)  
 CC antagonist. For treatment and prevention of diabetes, obesity, for  
 CC lowering blood sugar levels and for use in controlling appetite. The  
 CC present sequence represents a protein associated with growth hormone  
 CC secretagogue receptor.

Query Match 99.4%; Score 2141; DB 8; Length 412;  
 Best Local Similarity 99.5%; Pred. No. 8e-194;  
 Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFFLGALVPVTVAVCLCLFVVGSGNVTV 60  
 Db 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFFLGALVPVTVAVCLCLFVVGSGNVTV 60

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Qy 61 MLIGRYEDMETTNLYLGSMAVSDLLILLGLPFDLRLWRSRPWVFGPLLCLRLSLYVGE 120
Db 61 MLIGRYEDMETTNLYLGSMAVSDLLILLGLPFDLRLWRSRPWVFGPLLCLRLSLYVGE 120
Qy 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVLVGE 180
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVLVGE 180
Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLMLSRAPPPSPGPETAEEAALFSRECKRPSA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLMLSRAPPPSPGPETAEEAALFSRECKRPSA 240
Qy 241 QLGALRVMLWVTTAYFFLPCLLSIYGLIGRELWSSRRPLRGPASGRGRGHQTVRVL 300
Db 241 QLGALRVMLWVTTAYFFLPCLLSIYGLIGRELWSSRRPLRGPASGRGRGHQTVRVL 300
Qy 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Qy 361 KYRAAAFKLLAKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG 412
Db 361 KYRAAAFKLLAKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTMG 412

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Search completed: April 11, 2005, 21:02:39  
 Job time : 72.6667 secs

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OM protein - protein search, using sw model

Run on: April 11, 2005, 20:05:13 ; Search time 21.1679 Seconds  
(without alignments)  
1452.926 Million cell updates/sec

Title: US-09-719-485-3

Perfect score: 2155

Sequence: 1 MGSPWNGSDGEGAREPPWP.....DTGDTVGYTETSANVKMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*
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- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2155	100.0	412	US-09-743-742B-8	Sequence 8, Appli
2	865.5	40.2	349	US-09-762-661A-2	Sequence 2, Appli
3	864.5	40.1	366	US-09-762-661A-7	Sequence 7, Appli
4	864.5	40.1	366	US-09-743-475-6	Sequence 6, Appli
5	863.5	40.1	366	US-09-077-675A-13	Sequence 13, Appli
6	863.5	40.1	366	US-09-077-674-13	Sequence 13, Appli
7	863.5	40.1	366	US-09-170-496D-88	Sequence 8, Appli
8	863.5	40.1	366	US-09-743-742B-7	Sequence 7, Appli
9	863.5	40.1	366	US-09-762-661A-5	Sequence 5, Appli
10	863.5	40.1	366	US-09-364-425B-45	Sequence 45, Appli
11	863.5	40.1	366	US-09-743-475-4	Sequence 4, Appli
12	863	40.0	353	US-09-077-675A-3	Sequence 3, Appli
13	863	40.0	353	US-09-077-674-3	Sequence 3, Appli
14	861.5	40.0	364	US-09-077-675A-16	Sequence 16, Appli
15	861.5	40.0	364	US-09-077-674-16	Sequence 16, Appli
16	861.5	40.0	364	US-09-762-661A-6	Sequence 6, Appli
17	861.5	40.0	364	US-09-743-475-3	Sequence 3, Appli
18	861.5	40.0	364	US-09-743-475-5	Sequence 5, Appli
19	860	39.9	361	US-09-077-675A-8	Sequence 8, Appli
20	860	39.9	361	US-09-077-674-8	Sequence 8, Appli
21	857.5	39.8	366	US-09-170-496D-210	Sequence 210, App
22	775.5	36.0	302	US-09-077-675A-2	Sequence 2, Appli
23	775.5	36.0	302	US-09-077-674-2	Sequence 2, Appli
24	774.5	35.9	302	US-09-077-675A-7	Sequence 7, Appli
25	774.5	35.9	302	US-09-077-674-7	Sequence 7, Appli
26	674.5	31.3	271	US-09-077-675A-12	Sequence 12, Appli
27	674.5	31.3	271	US-09-077-674-12	Sequence 12, Appli

28	644.5	29.9	289	3	US-09-077-675A-10	Sequence 10, Appli
29	644.5	29.9	289	4	US-09-077-674-10	Sequence 10, Appli
30	633	29.4	289	3	US-09-077-675A-5	Sequence 5, Appli
31	633	29.4	289	4	US-09-077-674-5	Sequence 5, Appli
32	497	23.1	418	4	US-09-743-742B-5	Sequence 5, Appli
33	491	22.8	418	4	US-09-826-509-535	Sequence 535, App
34	485.5	22.5	403	4	US-09-170-496D-114	Sequence 114, App
35	485.5	22.5	403	4	US-09-743-742B-4	Sequence 4, Appli
36	485.5	22.5	403	4	US-09-743-742B-10	Sequence 10, Appli
37	483.5	22.4	403	4	US-09-170-496D-224	Sequence 224, App
38	483	22.4	415	4	US-09-341-016A-1	Sequence 1, Appli
39	479	22.2	415	4	US-09-545-944-2	Sequence 2, Appli
40	476	22.1	412	4	US-09-949-016-10101	Sequence 10101, A
41	466	21.6	353	1	US-08-118-270-45	Sequence 45, Appli
42	466	21.6	353	5	PCT-US93-08528-45	Sequence 45, Appli
43	457.5	21.2	405	4	US-09-743-742B-2	Sequence 2, Appli
44	457.5	21.2	405	4	US-09-743-742B-11	Sequence 11, Appli
45	413	19.2	410	3	US-08-858-876A-2	Sequence 2, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-743-742B-8

; Sequence 8, Application US/09743742B

; Patent No. 6599718

; GENERAL INFORMATION:

; APPLICANT: Liu, Qingyun

; APPLICANT: Howard, Andrew D.

; APPLICANT: McKee, Karen Kulju

; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED

; TITLE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS

; FILE REFERENCE: 20217YP

; CURRENT APPLICATION NUMBER: US/09/743,742B

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: PCT/US99/15941

; PRIOR FILING DATE: 1999-07-13

; PRIOR APPLICATION NUMBER: 60/092,623

; PRIOR FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 412

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-743-742B-8

Query Match 100.0%; Score 2155; DB 4; Length 412;  
Best Local Similarity 100.0%; Pred. No. 3.7e-177;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSPWNGSDGEGAREPPWPALPPCDERRCPPLGALVPVTAVCLCLFVVGVSGNVTV	60
Db	1	MGSPWNGSDGEGAREPPWPALPPCDERRCPPLGALVPVTAVCLCLFVVGVSGNVTV	60
Qy	61	MLIGRYDMRTTNYLGLSMAVSLLILGLPFDLYRLMRSRPMWFGPCLLCRLSLYVGE	120
Db	61	MLIGRYDMRTTNYLGLSMAVSLLILGLPFDLYRLMRSRPMWFGPCLLCRLSLYVGE	120
Qy	121	CTYATLHMTALSVERVLAICRPLRARVLVTRRRVRAIAVLWVALLSAGPFLVGVGE	180
Db	121	CTYATLHMTALSVERVLAICRPLRARVLVTRRRVRAIAVLWVALLSAGPFLVGVGE	180
Qy	181	ODRGISVVGGLNGTARTASSPLASSPPLWLSRAPPPSPSPETAALFSSRCRPSPA	240
Db	181	ODRGISVVGGLNGTARTASSPLASSPPLWLSRAPPPSPSPETAALFSSRCRPSPA	240
Qy	241	QLGARVLMVLTATYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL	300
Db	241	QLGARVLMVLTATYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL	300
Qy	301	LWVLAFFICWLPFHVGRIIYINTSDSRMMYFSQYFNIVALQLFVLSASINPILYNLSK	360





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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-743-475-6

Query Match      40.1%; Score 864.5; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 2.3e-66;
Matches 189; Conservative 55; Mismatches 104; Indels 71; Gaps 10;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPGALGVPTAVCLCLFVVGVSGN 56
DB 2 WNATPSEBPGNLTLPDLGWDAPPENDSLVBELLPLFTPLLAGVTATCATVALFVVVGIA 61
QY 57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLLCRLSLY 116
DB 62 LITMLVSRFRMRMTTNNLYLSSMAFSDLLIFLCMPDLDFRLWQYRPNLGNLLCKLPQF 121
QY 117 VGECTATLHMTALSVERVLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176
DB 122 VSECTYATVLTITALSVERVLAICFPLRAKVVTKGRVILVIMVAVAFCSAGPIFVL 181
QY 177 VGVQDPCISVVVGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
DB 182 VGVHEH-----NGT-----DPRD-----TNECR 199
QY 237 PS--PAQIGALRVMLVTTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASG---RER 291
DB 200 ATEFAVRSGLLTVMVWSSVFFLPVFLCTVLYSLIGRKLW---RRKGEAAVSGSLRDQ 256
QY 292 GHQTVRVLLVVLAFIICWLPFHVGRIIY---INTEDSRMYFSQYFNIVALQLFYLSA 348
DB 257 NHQTVKMLAVVFAFICWLPFHVGRIYLFPSKLEPGSVETIAQISQYCNLYSFVLYLSA 316
QY 349 SINPLYNLISKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVGYTETSAN 407
DB 317 AINPLYNIMSKYRAVAVFKLLGFPFQKLSLTKDESSR-----AWTESSIN 365

RESULT 5
US-09-077-675A-13
; Sequence 13, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-13

Query Match      40.1%; Score 863.5; DB 3; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPGALGVPTAVCLCLFVVGVSGN 56
DB 2 WNATPSEBPGNLTADLDWDASFGNDSLGDELLQLFPAPLLAGVTATCATVALFVVVGIA 61
QY 57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLLCRLSLY 116
DB 62 LITMLVSRFRMRMTTNNLYLSSMAFSDLLIFLCMPDLDFRLWQYRPNWFGDLCKLPQF 121
QY 117 VGECTATLHMTALSVERVLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176
DB 122 VSECTYATVLTITALSVERVLAICFPLRAKVVTKGRVILVIMVAVAFCSAGPIFVL 181
QY 177 VGVQDPCISVVVGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
DB 182 VGVHEH-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQIGALRVMLVTTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASGRGHR 294
DB 200 PTEFAVRSGLLTVMVWSSVFFLPVFLCTVLYSLIGRKLWRRRRRGDAVVGASLRDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
DB 260 QTVKMLAVVFAFICWLPFHVGRIYLFPSKLEPGSVETIAQISQYCNLYSFVLYLSA 319
QY 352 PILYNLISKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVGYTETSAN 407
DB 320 PILYNIMSKYRAVAVFKLLGFPFQKLSLTKDESSR-----AWTESSIN 365

RESULT 6
US-09-077-674-13
; Sequence 13, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/077,674
/ FILING DATE: 3-JUN-1998
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cocuzzo, Anna L.
/ REGISTRATION NUMBER: 42,452
/ REFERENCE/DOCKET NUMBER: 19589P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 732-594-1273
/ TELEFAX: 732-594-4720
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 366 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-077-674-13

Query Match          40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVVGSGN 56
DQ 2 WNA TPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGIAGN 61
QY 57 VVTWMLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPLLCRLSLY 116
DQ 62 LITMLVSVRFRELTNNLYLSSMAFSDLLIFLCMPLDLVRLQVYRPWPMFGLDCKLQF 121
QY 117 VGEGETATLLHMTALSVERYLAICRPLRARVLTTRRRVRLAIVLWAVALLSAGPFLFL 176
DQ 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVGINGLTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236
DQ 182 VGVHE-----NGT-----DP-W-----DTNECR 199
QY 237 PS--PAQLGALRWLVWTTAYFFLPFLCLSLIYLGILGELWSSRRPLRGPAASGRGHR 294
DQ 200 PTEFAVRSGLLTVMWVSSIFFLFVFCVLTLYSLIGRKLWRRRGDVAVGASLRDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
DQ 260 QTVKMLAVVVFAPILCWLPFHVGRLYFSKSPGPSLEIAQISQYCNLVSVFLYLSA IN 319
QY 352 PILYNLSKYYRAAFKLLARKSRPRGHRSDTAGEVAGDTGDTVGYTETSAN 407
DQ 320 PILYNIMSKYRVAVFRLGPEFPSQKSLTKDESSR-----AWTESSIN 365

RESULT 7
US-09-170-496D-88
/ Sequence 88, Application US/09170496D
/ Patent No. 6555339
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
/ FILE REFERENCE: AREN-0040
/ CURRENT APPLICATION NUMBER: US/09/170,496D
/ NUMBER OF INVENTION: 1
/ NUMBER OF SEQ ID NOS: 13

Query Match          40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVVGSGN 56
DQ 2 WNA TPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGIAGN 61
QY 57 VVTWMLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPLLCRLSLY 116
DQ 62 LITMLVSVRFRELTNNLYLSSMAFSDLLIFLCMPLDLVRLQVYRPWPMFGLDCKLQF 121
QY 117 VGEGETATLLHMTALSVERYLAICRPLRARVLTTRRRVRLAIVLWAVALLSAGPFLFL 176
DQ 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVGINGLTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236
DQ 182 VGVHE-----NGT-----DP-W-----DTNECR 199
QY 237 PS--PAQLGALRWLVWTTAYFFLPFLCLSLIYLGILGELWSSRRPLRGPAASGRGHR 294
DQ 200 PTEFAVRSGLLTVMWVSSIFFLFVFCVLTLYSLIGRKLWRRRGDVAVGASLRDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
DQ 260 QTVKMLAVVVFAPILCWLPFHVGRLYFSKSPGPSLEIAQISQYCNLVSVFLYLSA IN 319
QY 352 PILYNLSKYYRAAFKLLARKSRPRGHRSDTAGEVAGDTGDTVGYTETSAN 407
DQ 320 PILYNIMSKYRVAVFRLGPEFPSQKSLTKDESSR-----AWTESSIN 365

RESULT 8
US-09-743-742B-7
/ Sequence 7, Application US/09743742B
/ Patent No. 6599718
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Qingyun
/ APPLICANT: Howard, Andrew D.
/ APPLICANT: McKee, Karen Kulju
/ TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED
/ FILE REFERENCE: 20217P
/ CURRENT APPLICATION NUMBER: US/09/743,742B
/ PRIOR FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: PCT/US99/15941
/ PRIOR FILING DATE: 1999-07-13
/ PRIOR APPLICATION NUMBER: 60/092,623
/ PRIOR FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 7
/ LENGTH: 366
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-743-742B-7

Query Match          40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVVGSGN 56
DQ 2 WNA TPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGIAGN 61
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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/077,674
/ FILING DATE: 3-JUN-1998
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cocuzzo, Anna L.
/ REGISTRATION NUMBER: 42,452
/ REFERENCE/DOCKET NUMBER: 19589P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 732-594-1273
/ TELEFAX: 732-594-4720
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 366 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-077-674-13

Query Match          40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVVGSGN 56
DQ 2 WNA TPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGIAGN 61
QY 57 VVTWMLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPLLCRLSLY 116
DQ 62 LITMLVSVRFRELTNNLYLSSMAFSDLLIFLCMPLDLVRLQVYRPWPMFGLDCKLQF 121
QY 117 VGEGETATLLHMTALSVERYLAICRPLRARVLTTRRRVRLAIVLWAVALLSAGPFLFL 176
DQ 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVGINGLTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236
DQ 182 VGVHE-----NGT-----DP-W-----DTNECR 199
QY 237 PS--PAQLGALRWLVWTTAYFFLPFLCLSLIYLGILGELWSSRRPLRGPAASGRGHR 294
DQ 200 PTEFAVRSGLLTVMWVSSIFFLFVFCVLTLYSLIGRKLWRRRGDVAVGASLRDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
DQ 260 QTVKMLAVVVFAPILCWLPFHVGRLYFSKSPGPSLEIAQISQYCNLVSVFLYLSA IN 319
QY 352 PILYNLSKYYRAAFKLLARKSRPRGHRSDTAGEVAGDTGDTVGYTETSAN 407
DQ 320 PILYNIMSKYRVAVFRLGPEFPSQKSLTKDESSR-----AWTESSIN 365

RESULT 7
US-09-170-496D-88
/ Sequence 88, Application US/09170496D
/ Patent No. 6555339
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
/ FILE REFERENCE: AREN-0040
/ CURRENT APPLICATION NUMBER: US/09/170,496D
/ NUMBER OF INVENTION: 1
/ NUMBER OF SEQ ID NOS: 13

Query Match          40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVVGSGN 56
DQ 2 WNA TPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGIAGN 61
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RESULT 11

US-09-743-475-4  
; Sequence 4, Application US/09743475  
; Patent No. 6682908  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Roy G.  
; APPLICANT: Van der Ploeg, Leonardus H. T.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Zheng, Hui  
; APPLICANT: McKee, Karen Kulju  
; APPLICANT: Jiang, Michael M.  
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE  
; FILE REFERENCE: 20218P  
; CURRENT APPLICATION NUMBER: US/09/743,475  
; CURRENT FILING DATE: 2001-01-10  
; PRIOR APPLICATION NUMBER: PCT/US99/15375  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: 60/092,361  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-743-475-4

Query Match 40.1%; Score 863.5; DB 4; Length 366;  
Best Local Similarity 44.7%; Pred. No. 2.9e-66;  
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPCD-----ERRCSPFPGALVPVAVCLCLFVVGVSQN 56  
DB 2 WNAETSEPGFNLTADLDWDASPGNDSLGDELQLFAPPLIAGVTATCVALLFVVGIA 61  
QY 57 VVTVMILGVRDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPMVFGPLLCRLSLY 116  
DB 62 LUTMLVVSFRERITTNLYLSMAFSDLLIFLCPLDLVRLWQYRPNFGLLCKLPQF 121  
QY 117 VGECTYATLLHMTALSVERYLAICRPLRVLVTRRRVRLIALVLAVALLSAGPFLFL 176  
DB 122 VSECTYATVLTALSVERYFAICFPLRAKVVKIGRVKLVIFVIAVAFCSAGPIFVL 181  
QY 177 VGEQDPGIVVPGVGLNGTARIASSPLASSPPLWLRAPPPSPGPETAAALFSRECR 236  
DB 182 VGVHEH-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQLGALVLMVMTTAYFELPLCLSLYGLIGRELWSSRPLRGPAASGRGRHR 294  
DB 200 PTEFAVRSGLLTVMVWSIFFLPVFCVTLVLSLIGRLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTVRVLVVLVLAFCICWLPFHVGRITTYINTEDS---RMMYFSQYFNIVALQLFYLSASIN 351  
DB 260 QIVKMLAVVVFALICWLPFHVGRYLFKSPFGLSLEIAIQISQYCNLVSVFLFYLSA 319  
QY 352 PLYNLISKYRAAFKLLARKSRPGRHRSRDTAGEVAGDTGDTVGYTETSAN 407  
DB 320 PLYNIMSKYRVAVFRLIGFEPFSGQKSLTKDESSR-----AWTESSIN 365

RESULT 12

US-09-077-675A-3  
; Sequence 3, Application US/09077675A  
; Patent No. 6242199  
; GENERAL INFORMATION:  
; APPLICANT: Pai, Lee-Yuh  
; APPLICANT: Feigner, Scott C.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Pong, Sheng-Shung  
; APPLICANT: Van Der Ploeg, Leonardus H. T.

; TITLE OF INVENTION: RECEPTOR ASSAY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,675A  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19590P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 353 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-077-675A-3

Query Match 40.0%; Score 863; DB 3; Length 353;  
Best Local Similarity 46.5%; Pred. No. 3e-66;  
Matches 186; Conservative 53; Mismatches 95; Indels 66; Gaps 9;  
QY 19 WPALPPCD---ERRCSPFPGALVPVAVCLCLFVVGVSQNVVWMLIGRVRDMRTTNL 75  
DB 8 WDAPPENDSLVEELLPLFPPTLLAGVTATCVALLFVVGIAQNLTLMLVVSFRERITTNL 67  
QY 76 YLGSMAVSDLLILGLPFDLYRLWRSRPMVFGPLLCRLSLYVGECTYATLLHMTALSVE 135  
DB 68 YLSSMAFSDLLIFLCPLDLVRLWQYRPNLGNLLCKLPQFVSECTYATVLTITALSVE 127  
QY 136 RYLAICRPLRVLVTRRRVRLIALVLAVALLSAGPFLVGVGPQDPGISVVPGLNGTA 195  
DB 128 RYFALCFPLRAKVVKIGRVKLVIFVIAVAFCSAGPIFVLVGVHEH-----NGT- 177  
QY 196 RIASSPLASSPPLWLRAPPPSPGPETAAALFSRECRPS---PAQLGALVLMVMTT 253  
DB 178 -----DPRD-----TNECRATEFAVRSGLLTVMVWS 205  
QY 254 AYFFLPFLCLSLYGLIGRELWSSRPLRGPAASG---RERCHROTVRVLVVLAFILIC 310  
DB 206 VFFFLFVFCVTLVLSLIGRKLW---RRKRGAAVSSLRDQNHKQTVKMLAVVVFALIC 262  
QY 311 WLPFHVGRITTY---INTEDSRMMYFSQYFNIVALQLFYLSASINFLYNLISKYRAAF 367  
DB 263 WLPFHVGRYLFKSPFGLSLEIAIQISQYCNLVSVFLFYLSAINFILYNIMSKYRVAVF 322  
QY 368 KLLARKSRPGRHRSRDTAGEVAGDTGDTVGYTETSAN 407  
DB 323 KLLGFEPPFSGQKSLTKDESSR-----AWTESSIN 352

RESULT 13  
US-09-077-674-3

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; Sequence 3, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-674-3

Query Match 40.0%; Score 863; DB 4; Length 353;
Best Local Similarity 46.5%; Pred. No. 3e-66;
Matches 186; Conservative 53; Mismatches 95; Indels 66; Gaps 9;

Qy 19 WPALPPCD---ERRCSPPPLGALVPVAVCLFLVGVSGNVVTVMLIGRYEDMRTTNL 75
Db 8 WDAPENDSLVEELLPLFPTELLAGVATVATVAVGVGIAGNLLTMLVVSFRMRTTNL 67

Qy 76 YLGSMAVSDLLILGLPDLVRLWRSRPPVFGPLLCRLSLVVGECTVATLLHMTALSVE 135
Db 68 YLSSMAFSDLLIFLCMPDLDFRLWQYRPNLGNLLCKLFPQVSSRCTVATVLTALSVE 127

Qy 136 RYLAICRPLRVLVTRRRVRLIALVAVALLSAGPFLFVLGVQDPGISVFPGLNGTA 195
Db 128 RYFAICFPLRAKVVVTKGRVKLVILVAVAFCSAGPIFVLGVGEHD-----NGT- 177

Qy 196 RIASSPLASSPPLWLSRAPPPSPGPGPETAABALFSRECRPS--PAQLGALRVLMTWT 253
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVMVWVSS 205

Qy 254 AYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAAG---RRGRHQTIVRLVLLVWLAFIIC 310
Db 206 VFFLPFLVCLVLSLIGRKLW---RRKRGANVGSRLQDNHKTQVGMVAVVFAFILC 262

Qy 311 WLPFHVGRIIY---INTEDSRMVFSPQYFNIVNLQFLYLSASINPILYNLISKYRAAAF 367

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Db 263 WLPFHVGRIYFSKSLBPGSVIEIAQISQYCNLVSVFLYLSAAINPILYNIMSKYRVAVF 322
Qy 368 KLLARKSRPRGPHRSRDTAGEVAGDTGGDTGVGTETSAN 407
Db 323 KLLGFEPFSQKSLTKDESSR-----ANTESSIN 352

RESULT 14
US-09-077-675A-16
; Sequence 16, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-16

Query Match 40.0%; Score 861.5; DB 3; Length 364;
Best Local Similarity 48.3%; Pred. No. 4.2e-66;
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

Qy 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPPLGALVPVAVCLFLVGVSG 55
Db 2 WNAAT--PSEPEPNVTLDDWDASPGNDSLPLDELLPLFPAPLLAGVATVATVAVGVG 59

Qy 56 NVTVMLIGRYEDMRTTNLILGLPDLVRLWRSRPPVFGPLLCRLSL 115
Db 60 NLLTMLVVSFRMRTTNLILGLPDLVRLWQYRPNLGNLLCKLFPQVSSRCTVATVLTALS 119

Qy 116 YVGGCTVATLLHMTALSVERYLAICRPLRVLVTRRRVRLIALVAVALLSAGPFLF 175
Db 120 FVSECTVATVLTALSVERYLAICRPLRVLVTRRRVRLIALVAVALLSAGPFLF 179

Qy 176 LVGVQDPGISVFPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGPETAABALFSREC 235

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Db 180 LVGVEHE-----NGT-----DPD-----TNEC 197
QY 236 RPS--PAQGLARVLMWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG---RE 290
Db 198 RATEFAVRSGLLTVMWVSSVFFLPVFCLTLYSLIGRKLW--RR--RGDAAVGASLRD 253
QY 291 RGHRTQVRVLLVVLAFILCWLPHVGRIRIYINTEDS---RMMYFSQVFNIVALQLFVLS 347
Db 254 QNHKQTVKMLAVVVFALICWLPHVGRYLFKSPGSLTAQISQYCNLVSVFLVLS 313
QY 348 ASINPILYNLSKKYRAAFKLL 370
Db 314 AAINPILYNIMSKKYRVAVFKLL 336

RESULT 15
US-09-077-674-16
; Sequence 16, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-674-16
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Query Match 40.0%; Score 861.5; DB 4; Length 364;  
Best Local Similarity 48.3%; Pred. No. 4.2e-66;  
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

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QY 5 WNGSDGPEGAREP-----PWPALPPC-----ERRCSPEPLGALVPVTAVCLCLFVVGVS 55
Db 2 WNAT--PSEEPFNVTLDWDASFGNDSLPDELLPLFPALLAGTATCATVALFVVGISG 59
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QY 56 NVVTMLIGRYDRMTTNNLYLGSWAYSDLLILGLPEDLYLWRSRPWVFGPLICRLSL 115
Db 60 NLLTMLVVSRRPRELRTTNNLYLSSMAFSDLLIFLCMPDLDLVRLWQYRPWNFGDLLCKLFQ 119
QY 116 YVGBGCTYATLLHMTALSVERYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPPLF 175
Db 120 FVSESCIYATVLTITALSVERYPAICPLRAKVVTGKRVKLVILVIWAVAFCSAGPIFV 179
QY 176 LVGVEQDPGISVVPGLNGTARIASSPLASSPPLMLSRAPPPSPGPGTETAAAAALFSREC 235
Db 180 LVGVEHE-----NGT-----DPD-----TNEC 197
QY 236 RPS--PAQGLARVLMWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG---RE 290
Db 198 RATEFAVRSGLLTVMWVSSVFFLPVFCLTLYSLIGRKLW--RR--RGDAAVGASLRD 253
QY 291 RGHRTQVRVLLVVLAFILCWLPHVGRIRIYINTEDS---RMMYFSQVFNIVALQLFVLS 347
Db 254 QNHKQTVKMLAVVVFALICWLPHVGRYLFKSPGSLTAQISQYCNLVSVFLVLS 313
QY 348 ASINPILYNLSKKYRAAFKLL 370
Db 314 AAINPILYNIMSKKYRVAVFKLL 336
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Search completed: April 11, 2005, 21:06:22  
Job time : 23.1679 secs

1	2155	100.0	412	14	US-10-225-567A-473	Sequence 473, Appl
2	2155	100.0	412	14	US-10-290-078-15	Sequence 15, Appl
3	2155	100.0	412	14	US-10-318-661-28	Sequence 28, Appl
4	2155	100.0	412	14	US-10-206-677-2	Sequence 2, Appl
5	2149	99.7	412	10	US-09-876-252-130	Sequence 130, App
6	2149	99.7	412	15	US-10-417-820A-130	Sequence 130, App
7	2149	99.7	412	15	US-10-417-820A-150	Sequence 150, App
8	2149	99.7	412	16	US-10-723-955-130	Sequence 130, App
9	863.5	40.1	366	14	US-10-251-385-88	Sequence 88, Appl
10	863.5	40.1	366	14	US-10-303-204A-13	Sequence 13, Appl
11	863	40.0	353	14	US-10-303-204A-3	Sequence 3, Appl
12	861.5	40.0	361	14	US-10-303-204A-16	Sequence 16, Appl
13	860	39.9	361	14	US-10-303-204A-8	Sequence 8, Appl

Db 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
QY 181 QPGLSVVPLNGTARIASSPPLASPPPLWLSRAPPPSPGPTAAALFSRECRPSA 240  
Db 181 QPGLSVVPLNGTARIASSPPLASPPPLWLSRAPPPSPGPTAAALFSRECRPSA 240  
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
QY 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTGM 412  
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTGM 412

## RESULT 2

US-10-290-078-15  
; Sequence 15, Application US/10290078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; FILE REFERENCE: 14395, 14618, 17692 or 58874  
; CURRENT APPLICATION NUMBER: US/10/290,078  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-290-078-15

Query Match 100.0%; Score 2155; DB 14; Length 412;  
Best Local Similarity 100.0%; Pred. No. 2.6e-167;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
QY 61 MLIGRYDRMRTTNNLYGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 120  
Db 61 MLIGRYDRMRTTNNLYGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 120  
QY 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
Db 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
QY 181 QPGLSVVPLNGTARIASSPPLASPPPLWLSRAPPPSPGPTAAALFSRECRPSA 240  
Db 181 QPGLSVVPLNGTARIASSPPLASPPPLWLSRAPPPSPGPTAAALFSRECRPSA 240  
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
QY 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTGM 412  
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTGM 412

## RESULT 3

US-10-318-661-28  
; Sequence 28, Application US/10318661  
; Publication No. US20030167476A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Bruce R.  
; TITLE OF INVENTION: Selective Target Cell Activation By  
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
; FILE REFERENCE: UCAL-049CIP2  
; CURRENT APPLICATION NUMBER: US/10/318,661  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: US 09/341,446  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US97/05334  
; PRIOR FILING DATE: 1997-03-25  
; PRIOR APPLICATION NUMBER: US 08/622,348  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-318-661-28

Query Match 100.0%; Score 2155; DB 14; Length 412;  
Best Local Similarity 100.0%; Pred. No. 2.6e-167;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
QY 61 MLIGRYDRMRTTNNLYGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 120  
Db 61 MLIGRYDRMRTTNNLYGSMVSDLLILLGLPFDLYRLWRSRPWVFGPILLCRLSLYVGE 120  
QY 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
Db 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180  
QY 181 QPGLSVVPLNGTARIASSPPLASPPPLWLSRAPPPSPGPTAAALFSRECRPSA 240  
Db 181 QPGLSVVPLNGTARIASSPPLASPPPLWLSRAPPPSPGPTAAALFSRECRPSA 240  
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300  
QY 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
Db 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTGM 412  
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTGM 412

## RESULT 4

US-10-206-677-2  
; Sequence 2, Application US/10206677  
; Publication No. US20030186336A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences, Inc.  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; APPLICANT: Kulaender, Bruce G.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO  
; TITLE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)  
; FILE REFERENCE: 1920-1-8  
; CURRENT APPLICATION NUMBER: US/10/206,677



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; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-206-677-2

Query Match      100.0%; Score 2155; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVVGSGNVTV 60
Db      1  MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVVGSGNVTV 60

Qy      61  MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
Db      61  MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120

Qy      121  CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180
Db      121  CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180

Qy      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTETAAALFSRECRPSPA 240
Db      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTETAAALFSRECRPSPA 240

Qy      241  QLGLARVLMVWTTAVFFPELCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
Db      241  QLGLARVLMVWTTAVFFPELCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300

Qy      301  LVVLAFTICWLPFHVGRIIINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLSK 360
Db      301  LVVLAFTICWLPFHVGRIIINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLSK 360

Qy      361  KYRAAFKLLARKSRPRGFRHSRTAGEVAGDTGDTGVGTETTSANYKTWG 412
Db      361  KYRAAFKLLARKSRPRGFRHSRTAGEVAGDTGDTGVGTETTSANYKTWG 412

RESULT 5
US-09-876-252-130
; Sequence 130, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26

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; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-130

Query Match      99.7%; Score 2149; DB 10; Length 412;
Best Local Similarity 99.8%; Pred. No. 7.9e-167;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVVGSGNVTV 60
Db      1  MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVVGSGNVTV 60

Qy      61  MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
Db      61  MLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120

Qy      121  CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180
Db      121  CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180

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QY 61 MLIGRYDMRTTNNLYGSMVSDLLILLGLPFDLYRLWRSRPWVFGPCLLCRLSLYVGEG 120  
Db 61 MLIGRYDMRTTNNLYGSMVSDLLILLGLPFDLYRLWRSRPWVFGPCLLCRLSLYVGEG 120  
QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180  
Db 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTQKRVL 300  
Db 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTQKRVL 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFVLSASINPILYNLISK 360  
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFVLSASINPILYNLISK 360  
QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412  
Db 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

## RESULT 8

US-10-723-955-130  
; Sequence 130, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinsma, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US29.CON  
; CURRENT APPLICATION NUMBER: US/10/723,955  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 10/417,820  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 130  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-10-723-955-130

Query Match 99.7%; Score 2149; DB 16; Length 412;  
Best Local Similarity 99.8%; Pred. No. 7.9e-167;  
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPFLGALVPVTAIVCLCLFVVGVSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPFLGALVPVTAIVCLCLFVVGVSGNVTV 60  
QY 61 MLIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPCLLCRLSLYVGEG 120  
Db 61 MLIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPCLLCRLSLYVGEG 120  
QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180  
Db 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTQKRVL 300  
Db 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTQKRVL 300  
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFVLSASINPILYNLISK 360  
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFVLSASINPILYNLISK 360  
QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412  
Db 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

## RESULT 9

US-10-251-385-88  
; Sequence 88, Application US/10251385  
; Publication No. US20030105292A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G  
; TITLE OF INVENTION: Protein-Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/10/251,385  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: US/09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-251-385-88

Query Match 40.1%; Score 863.5; DB 14; Length 366;  
Best Local Similarity 44.7%; Pred. No. 4.2e-62;  
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;  
QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPFLGALVPVTAIVCLCLFVVGVSGN 56  
Db 2 WNATPSEBPGFNLTADLDWDASFGNDSGLDELQLQFPAPLAGVTATCATVALFVVGIA 61  
QY 57 VVTVMILIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPCLLCRLSLY 116  
Db 62 LITMLVWSRPRELRTTNNLYLSSMAFSDLLIFLCWPLDLVRLWQYRPNWFGDLCKLQF 121  
QY 117 VEGCTATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFL 176

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Db 122 VSECTYATVLTITALSVERYFAICPLRAKVVVTKGRVCLVIFVIWAVFCSAGPIFVL 181
QY 177 VGVQDPGIVSVVGLNGTARIASSPLASSPPLWLRAPPSPSPGPTAEAAALFSRECR 236
Db 182 VGVHEH-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQLGALRVMLVVTAYFPLPCLISILYGLIGRELWSSRRPLRGPAAASGRGRHR 294
Db 200 PTEFAVRSGLLTVWVWSSIFFLPVCLTVLSIGRLWRRRGDVAVGASLDDQNHK 259
QY 295 QTVRVLVVLAFIICWLPFHVGRRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVVFALICWLPFHVGRVLFKSPGSLTAQISQYCNLVSVFLFYLAAIN 319
QY 352 PLYNLSKYYRAAFKLLARKSRPGRFHRSDRTAGEVAGDTGGDTVGYTETSAN 407
Db 320 PLYNIMSKKYRAVAVFRLGPFPSQKSLTKDESSR-----AWTESSIN 365

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## RESULT 10

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US-10-303-204A-13
; Sequence 13, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 366
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-303-204A-13

```

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Query Match 40.1%; Score 863.5; DB 14; Length 366;
Best Local Similarity 44.7%; Pred. No. 4.2e-62;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDQPEGA-----REPWPALPPCD---ERRCSPFPLGALVPVTVACLCIFVVGSGN 56
Db 2 WNAITSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATCVALFVVGIAGN 61
QY 57 VTVMLIGRYDRMTTNNLYLGSMAVSDLLILGLPDLVLRWRSRPVFGPCLLCRLSLY 116
Db 62 LLTMLVSRFRELRTTNNLYLSSMAFSDLLIFLCMPDLVLRWQYRPNWFGDLLCKLQF 121
QY 117 VCEGCTYATLLHWTALSVERYLAICRPLARVLTTRVRALVAVALLSAGPFLFL 176
Db 122 VSECTYATVLTITALSVERYFAICPLRAKVVVTKGRVCLVIFVIWAVFCSAGPIFVL 181
QY 177 VGVQDPGIVSVVGLNGTARIASSPLASSPPLWLRAPPSPSPGPTAEAAALFSRECR 236
Db 182 VGVHEH-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQLGALRVMLVVTAYFPLPCLISILYGLIGRELWSSRRPLRGPAAASGRGRHR 294

```

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Db 200 PTEFAVRSGLLTVWVWSSIFFLPVCLTVLSIGRLWRRRGDVAVGASLDDQNHK 259
QY 295 QTVRVLVVLAFIICWLPFHVGRRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVVFALICWLPFHVGRVLFKSPGSLTAQISQYCNLVSVFLFYLAAIN 319
QY 352 PLYNLSKYYRAAFKLLARKSRPGRFHRSDRTAGEVAGDTGGDTVGYTETSAN 407
Db 320 PLYNIMSKKYRAVAVFRLGPFPSQKSLTKDESSR-----AWTESSIN 365

RESULT 11
US-10-303-204A-3
; Sequence 3, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-3

```

```

Query Match 40.0%; Score 863; DB 14; Length 353;
Best Local Similarity 46.5%; Pred. No. 4.4e-62;
Matches 186; Conservative 53; Mismatches 95; Indels 66; Gaps 9;

QY 19 WPALPPCD---ERRCSPFPLGALVPVTVACLCIFVVGSGNVVTVMLIGRYDRMTTNNL 75
Db 8 WDAPPENDSLVEELLPLFPPTPLAGVATCVALFVVGIAGNLLTMLVSRFRELRTTNNL 67
QY 76 YLGSMAVSDLLILGLPDLVLRWRSRPVFGPCLLCRLSLYVVGCTYATLLHWTALSVE 135
Db 68 YLSSMAFSDLLIFLCMPDLVLRWQYRPNWLNLLCKLQFVSVSCTYATVLTITALSVE 127
QY 136 RYLAICRPLARVLTTRVRALVAVALLSAGPFLVGVQDPGIVSVVPLNGTA 195
Db 128 RYFAICRPLARVLTTRVRALVAVALLSAGPFLVGVQDPGIVSVVPLNGTA 177
QY 196 RIASSPLASSPPLWLRAPPSPSPGPTAEAAALFSRECRPS--PAQLGALRVMLVWTT 253
Db 178 -----DPRD-----TNECRATFAVRSGLLTVWVWSS 205
QY 254 AYFPLPCLISILYGLIGRELWSSRRPLRGPAAAG---RRGHRQTVRVLVVLAFIIC 310
Db 206 VFFELPVCLTVLSIGRLW---RRKRGAAVGSLSLDDQNHKQTVKMLAVVVFALIC 262
QY 311 WLPFHVGRRIIY---INTEDSRMVFSQYFNIVALQLFYLSASINPILYNLSKYYRAAF 367
Db 263 WLPFHVGRVLFKSPGSLTAQISQYCNLVSVFLFYLAAINPILYNLSKYYRAAF 322

```

QY 368 KILLARKSPRGHRSRDTAGEVAGDTGDTGVGYTETSAN 407  
Db 323 KLLGFEPFSQKSLTLKDESSR-----AWTESSIN 352

## RESULT 12

US-10-303-204A-16  
; Sequence 16, Application US/10303204A  
; Publication No. US20030166144A1  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus H. T.  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR  
; TITLE OF INVENTION: FAMILY  
; FILE REFERENCE: 19589PCA  
; CURRENT APPLICATION NUMBER: US/10/303,204A  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 09/077,674  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: PCT/US96/19445  
; PRIOR FILING DATE: 1996-12-10  
; PRIOR APPLICATION NUMBER: 60/018,962  
; PRIOR FILING DATE: 1996-06-06  
; PRIOR APPLICATION NUMBER: 60/008,582  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: rattus norvegicus

US-10-303-204A-16

Query Match 40.0%; Score 861.5; DB 14; Length 364;  
Best Local Similarity 48.3%; Pred. No. 6.1e-62;  
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

QY 5 WNGSDGPEGARP-----PWALPPCD-----ERRCSPPPLGALVPVTAVCLCLFVGVSG 55  
Db 2 WNAT--PSEEPFNVTLDDWDASPGNDSLDELPLFPAPLAGVTATCVAFVVGISG 59  
QY 56 NVVTVMILGRYDMMTTNLYLGSMAVSDLLILGLPDLVLRWSRWVFGPGLLCRLSL 115  
Db 60 NLLTMLVSVRFRELTITNLYLSSWAFSDLLIFLCMPDLVLRWQYRPWNFGDLLCKLPQ 119  
QY 116 YVGECTYATLHMTALSVERYLAICRPLRVLVTRRRVRLALIAVLWAVALLSAGPELF 175  
Db 120 FVSECTYATVLTITALSVERYFAICPLRAKVVTKGRVKLVILVIAWAFCSAGPIFV 179  
QY 176 LVGEQDQGISVVPGLNGTARTIASSPLASSPPLWLSRAPPPSPGPGTAAALFSREC 235  
Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197  
QY 236 RPS--PAQGLARVLMWTTAYFFLPFLCLSLYLGLIGRELWSSRRPLRGPASG--RE 290  
Db 198 RATEFAVRSGLLTVMVWSSVFFFLVFLCTLVLYSLIGRKLW--RR--RGDAAVGASLRD 253  
QY 291 RGHQTVRLVLLVLAFLAICMLPPHVGRIIYINTEDS---RMVFSQYFNIVALQLFVLS 347  
Db 254 QNHQTVKMLAVVFAFLLCMLPFHVGRLYFSKSPFGSLEIAQISQYCNLVSVFLVLS 313  
QY 348 ASINPILYNLSKKYRAAFKLL 370  
Db 314 AAINPILYNLSKKYRVAVFKLL 336

## RESULT 13

US-10-303-204A-8

; Sequence 8, Application US/10303204A  
; Publication No. US20030166144A1  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus H. T.  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR  
; TITLE OF INVENTION: FAMILY  
; FILE REFERENCE: 19589PCA  
; CURRENT APPLICATION NUMBER: US/10/303,204A  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 09/077,674  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: PCT/US96/19445  
; PRIOR FILING DATE: 1996-12-10  
; PRIOR APPLICATION NUMBER: 60/018,962  
; PRIOR FILING DATE: 1996-06-06  
; PRIOR APPLICATION NUMBER: 60/008,582  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: homo sapiens

US-10-303-204A-8

Query Match 39.9%; Score 860; DB 14; Length 361;  
Best Local Similarity 46.1%; Pred. No. 8e-62;  
Matches 183; Conservative 57; Mismatches 97; Indels 60; Gaps 8;

QY 19 WPALPPCD-----ERRCSPPPLGALVPVTAVCLCLFVGVSGNVVTVMILGRYDMMTTN 75  
Db 16 WDASPGNDSLGLDELILQLFPAPLAGVTATCVAFVVGIAGNLLTMLVSVRFRELTITN 75  
QY 76 YLGSMAVSDLLILGLPDLVLRWSRWVFGPGLLCRLSLYVGECTYATLHMTALSVE 135  
Db 76 YLSSWAFSDLLIFLCMPDLVLRWQYRPWNFGDLLCKLPFVSECTYATVLTITALSVE 135  
QY 136 RYLAICRPLRVLVTRRRVRLALIAVLWAVALLSAGPELFVGVQDQGISVVPGLNGTA 195  
Db 136 RYFAICPLRAKVVTKGRVKLVIFVIAWAFCSAGPIFVLGVGE-----NGT- 185  
QY 196 RIASSPLASSPPLWLSRAPPPSPGPGTAAALFSRECRPS--PAQGLARVLMWTT 253  
Db 186 -----DP--W-----DTNECRPTEPAVRSGLLTVMVWVSS 213  
QY 254 AYFFLPFLCLSLYLGLIGRELWSSRRPLRGPASGRBGRHQTVRVLLVVLAFIICWLP 313  
Db 214 IFFLPFVCLVLVSLIGRKLWRRRGDAVVGASURDQNHQTVKMLAVVFAFLLCMLP 273  
QY 314 FHVGRRIIYINTEDS---RMVFSQYFNIVALQLFVLSASINPILYNLSKKYRAAFKLL 370  
Db 274 FHVGRYLFKSPFGSLEIAQISQYCNLVSVFLVLSAIPILYNLSKKYRVAVFKLL 333  
QY 371 LARKSRPGRFHRSDRTAGEVAGDTGGDTGVGYTETSAN 407  
Db 334 GFEPFSQKSLTKDESSR-----AWTESSIN 360

## RESULT 14

US-10-251-385-210  
; Sequence 210, Application US/10251385  
; Publication No. US20030105292A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G

```
; TITLE OF INVENTION: Protein-Coupled
; FILE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 210
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-210

Query Match      39.8%; Score 857.5; DB 14; Length 366;
Best Local Similarity 44.5%; Pred. No. 1.3e-61;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY  5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAACLCLFVVGVSGN 56
DB  2 WNAFSEBPGFNLTADLDWDASPNDSLGDELLQLFPAPLLAGVTATCVAFVVVGIAQN 61

QY  57 VVTVMILGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGELLCRLSLY 116
DB  62 LLTMLVSRFRRLTNNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLQF 121

QY  117 VQEGCTATLLHMTALSVERYLAICRPLARVLVTRRRVRLIALVLAVALLSAGPFLFL 176
DB  122 VSESCTATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181

QY  177 VQVEODPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
DB  182 VQVEHE-----NGT-----DP--W-----DTNECR 199

QY  237 PS--PAQLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRLRGPAAASGRGHR 294
DB  200 PTEFAVRSGLLTVWVWSSVFFLPVCLTVLSYLGRLKRRRGDAVVGASLRDQNHK 259

QY  295 QTVRVLLVVLAFIICWLPFHVGRIIYNTEDS---RMVFSQYFNIVALQLFYLASIN 351
DB  260 QTKMLAVVVFAPILCWLPFHVGRLFSKSLPFGSLIAQISQYCNLVSVFLYLSAAN 319

QY  352 PILYNLSKKYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTVGYTETSAN 407
DB  320 PILYNMSKKYRVAVFRLIGPFPFSQKSLTKDESSR-----AWTESSIN 365

RESULT 15
US-10-303-204A-2
; Sequence 2, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
```

```
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 302
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-2

Query Match      36.0%; Score 775.5; DB 14; Length 302;
Best Local Similarity 46.6%; Pred. No. 5e-55;
Matches 166; Conservative 48; Mismatches 79; Indels 63; Gaps 8;

QY  60 VMLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPCLLCRLSLYVGE 119
DB  1 MLVVSFRFRMTTNNLYLSSMAFSDLLIFLCMPDLFRLWQYRPNWNLGNLICKLQFVSE 60

QY  120 GCTVATLLHMTALSVERYLAICRPLARVLVTRRRVRLIALVLAVALLSAGPFLVLGV 179
DB  61 SCTVATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVILVIMAVAFCSAGPIFVLGV 120

QY  180 BODPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPS- 238
DB  121 EHD-----NGT-----DPRD-----TNECRATE 138

QY  239 -PAQLGALRVMLWVTYAYFFLPCLSLIYGLIGRELWSSRRLRGPAAASG---RERGHR 294
DB  139 FAVRSGLLTVWVWSSVFFLPVCLTVLSYLGRLKRW---RRKRGEAAVGSRLRDQNHK 195

QY  295 QTVRVLLVVLAFIICWLPFHVGRIIY---INTEDSRMVFYSOYFNIVALQLFYLASIN 351
DB  196 QTVKMLAVVVFAPILCWLPFHVGRLFSKSLPFGSLIAQISQYCNLVSVFLYLSAAN 255

QY  352 PILYNLSKKYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTVGYTETSAN 407
DB  256 PILYNMSKKYRVAVFRLIGPFPFSQKSLTKDESSR-----AWTESSIN 301

Search completed: April 11, 2005, 21:21:24
Job time : 237.977 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2005, 19:24:50 ; Search time 17.5539 Seconds  
(without alignments)  
2258.264 Million cell updates/sec

Title: US-09-719-485-3  
Perfect score: 2155  
Sequence: 1 MGSPWNGSDGEGAREPPWP.....DTGGDTGVGTTSANVTMG 412

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	23.2	424	2	JH0164
2	497	23.1	418	2	S29506
3	453	21.0	477	2	JC7913
4	437	20.3	418	2	A88013
5	420	19.5	595	2	JC8012
6	401	18.6	416	2	S68822
7	392	18.2	658	2	JC8011
8	375	17.4	378	2	T15816
9	359	16.7	363	2	I57940
10	357.5	16.6	418	2	A46226
11	344	16.0	363	2	I57955
12	344	16.0	364	2	JN0763
13	343.5	15.9	380	2	A55259
14	339	15.7	352	2	JE0296
15	339	15.7	380	2	S36143
16	335	15.5	380	2	JC2338
17	335	15.5	388	2	JN0605
18	334.5	15.5	367	2	JC2421
19	334.5	15.5	367	2	I49022
20	334.5	15.5	367	2	I56520
21	334.5	15.5	428	2	S30508
22	331.5	15.4	428	2	A44021
23	330.5	15.3	370	2	S43087
24	329	15.3	380	2	A48227
25	328	15.2	380	2	JC2434
26	327.5	15.2	384	2	A47249
27	326.5	15.2	372	2	I38532
28	326	15.1	519	2	S17783
29	322	14.9	384	2	JC4629

Query Match	23.2%	Score 501;	DB 2;	Length 424;
Best Local Similarity	32.9%;	Pred. NO. 1.5e-32;		
Matches 125;	Conservative 59;	Mismatches 110;	Indels 86;	Gaps 11;
Qy	39	VPVTAVCICLVGVGNGVNVTVMLIGR---	YRDMRTTNLYLGSMVADLLI-LIGLPPD	94
Db	65	VLVTAIYALFVGVGVGNSVTAFTLARKKSLQSLQSTVHYHLGSLSDLLILLAMPVE	124	
Qy	95	LYR-LWRSRPVWFGPCLRLSLYVGEGETATLHMTALSVERYLAI CRPLARVLVTRR	153	
Db	125	LYNFIWVHPAFGDAGCGYFFLDADCTATALNVASLSVERYLAI CHPPKAKTLMRS	184	
Qy	154	RVRALIAVLWAVALLSAGFFFLVGVGEODPGISVVVPLNGTARTIASSPLASSPPLWLSRA	213	
Db	185	RTKKFISAILWLASALLAIPMLFTMGLQNRSGDTHPG-----GLVCTPIVDI	231	
Qy	214	PPPPSPGPTAEAAALFSPRCRSPAQGLGALRWMLWTTAYFFEL-PELCISILYGLIGR	272	
Db	232	-----ATVKVVIQNTFMSPFLFPMVLISILMTVAN	262	
Qy	273	ELWSSRRPLRGPAASGR-----ERGHRTVR-----VLLVVVLAFTI	309	
Db	263	KLTM-----VHQAEQGRVCTVGTNGLHSHSTFNTEIPGRVQALRHGVLEAVVAFV	319	
Qy	310	CWLPPHVGRIIYINTEDSR-----MMYFSQYFNIVALQLFYLSASINPILYNLISKYRAA	365	

#### ALIGNMENTS

##### RESULT 1

JH0164

neurotensin receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

C:Accession: JH0164

R:Tanaka, K.; Masu, M.; Nakanishi, S.

Neuron 4, 847-854, 1990

A:Title: Structure and functional expression of the cloned rat neurotensin receptor.

A:Reference number: JH0164; MUID:90297956; PMID:1694443

A:Accession: JH0164

A:Molecule type: mRNA

A:Residues: 1-424 <TAN>

A:Cross-references: UNIPROT:P20789

C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. The

ter (neuromodulator in the brain and as a hormone) cellular mediator in peripheral tiss

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:65-87/Domain: transmembrane #status predicted <TM1>

F:97-121/Domain: transmembrane #status predicted <TM2>

F:144-165/Domain: transmembrane #status predicted <TM3>

F:189-210/Domain: transmembrane #status predicted <TM4>

F:236-260/Domain: transmembrane #status predicted <TM5>

F:303-330/Domain: transmembrane #status predicted <TM6>

F:348-372/Domain: transmembrane #status predicted <TM7>

F:4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Db 320 CWLPHVRRMLFCYISDEQWTFLLDFYHYFMYLNFALFYSSAINPILYNLSANFRQV 379  
QY 366 AFKLLA-----RKSRP 377  
Db 380 FLSTLACLCPGWRHRRKKRP 399

RESULT 2  
S29506  
neurotensin receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S29506  
R.Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, D.; le F  
FEBS Lett. 317, 139-142, 1993  
A:Title: Cloning and expression of a complementary DNA encoding a high affinity human ne  
A:Reference number: S29506; MUID:93154505; PMID:8381365  
A:Accession: S29506  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-418 <VIT>  
A:Cross-references: UNIPROT:P30989; EMBL:X70070; NID:g35020; PIDN:CAA49675.1; PID:g35021  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 23.1%; Score 497; DB 2; Length 418;  
Best Local Similarity 33.1%; Pred. No. 3.le-32;  
Matches 126; Conservative 62; Mismatches 117; Indels 76; Gaps 13;  
QY 39 VPVTAVCLCLFVVGSGNVVTVMLIGR---YRDMRTTNLYLGSMAVSDLL-ILGLLPFD 94  
Db 64 VLVTAVLALFVVGTVGNTVTAFTLARKKSLQSLQSTVHYHLSLSDLLTLLAMPVE 123  
QY 95 LYR-LWRSRPWVFGPCLCLSLYVGEQCTYATLLHMTALSERYLAICRPARVLVTRR 153  
Db 124 LYNFIWVHPWAFGDCRGYFLRDACTYATALNVAASLSVRYLAICHPFKAKTLMGRS 183  
QY 154 RYRALIAVLWALLSAGPFLVGVQDPGIVSVVPLNGTARIASSPLASSPPLWLSRA 213  
Db 184 RTKKFISAIWLASALTVPMLFTMG-EQN----- 211  
QY 214 PPPSPSGPETAEEAALFSECRCPAQGLGARVLMWVTT-AYFFLPFLCLSLYGLIGR 272  
Db 212 -----RSADGQHAGLVCTPT-IHTATVKVIVQNTFMSFIPPMVVISVLTIAN 261  
QY 273 ELWSSRRPL--RGPAAS-----GREGRHQTIVRLVVLVLAFLICWLPFHV 316  
Db 262 KLTVMVRQAEOQCVCTVGGEHSTFSMAIEPGRVQALRHGVRVLRVAVIAFVVCWLPXV 321  
QY 317 GRIIYINTEDSR---MMY-FSOYENIVALQLFVLSASINPILYNLISKYR-----AA 365  
Db 322 RLKMPICYISDEQWTFPLDYHYFYFMYTNALFVSSINPILYNLSANFRHIFLATLAC 381  
QY 366 AFKLLARKSRPGRFHSRDT 386  
Db 382 LCPVWRERRKRP-AFSRKADS 401

RESULT 3  
JC7913  
capa receptor (CG14575) - fruit fly (Drosophila sp.)  
C:Species: Drosophila sp.  
C:Date: 31-Mar-2003 #sequence\_revision 31-Mar-2003 #text\_change 14-Jul-2003  
C:Accession: JC7913  
Riversen, A.; Cazzamali, G.; Williamson, M.; Hauser, F.; Grimmelikhuijzen, C.J.P.  
Biochem. Biophys. Res. Commun. 299, 628-633, 2002  
A:Title: Molecular cloning and functional expression of a Drosophila receptor for the ne  
A:Reference number: JC7913; MUID:22347021; PMID:12459185  
A:Accession: JC7913  
A:Molecule type: mRNA  
A:Residues: 1-477 <IVE>  
A:Cross-references: GB:AF505865

C:Comment: This receptor that is a G-protein-coupled receptor stimulates renal (Malpighi)  
C:Genetics:  
A:Introns: 70/3; 121/2; 126/1; 218/2; 276/2; 301/2; 349/1; 402/3; 436/3

Query Match 21.0%; Score 453; DB 2; Length 477;  
Best Local Similarity 29.7%; Pred. No. 1.2e-28;  
Matches 117; Conservative 68; Mismatches 135; Indels 74; Gaps 11;

QY 8 SDGEGAREPWPALPPCDERRCSP-----FPLGALVPVTAVCLCLFVVGSG 55  
Db 30 SDPSHGFGGEEDY----ACGTNFCSPKEVAVFLGPQTLPYKAVLITIFGGIFITVVG 85  
QY 56 NVVTVMLIGRYDRMRTTNLYLGSMAVSDLLIL-LGLPFDLYRLWRSRPWVFGPILCLRLS 114  
Db 86 NLLVCIVIRSAMHETATNYLFSLSAVSDLLYLLFGLTEVFLYWHQYDPLFGMPFCKIR 145  
QY 115 LYVGEQCTYATLLHMTALSERYLAICRPARVLVTRRRVRLIAVLWALLSAGPFL 174  
Db 146 AFISEACTYVSVFTVAFPSMERFLAICHPFLHYAMVGFKRAIRITITALLWIVSFISAIPP- 204  
QY 175 FLVGVQDPGIVSVVPLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRE 234  
Db 205 -----GLLSDIQYLNYPDHS-----RIEESAF----- 227  
QY 235 CRPSPAQLGARVLMWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRG--PAASGRERG 292  
Db 228 CSMSPKIVNEIPVEVSFCIFFVIPMILIILLYGRMGAKIRSRTNQKLVGQOQTNNRTR 287  
QY 293 HRQ-----TVRVLLVVVLAFLICWLPFHVGRIIYINTEDSRMYPFSQFNI-----VAL 341  
Db 288 NSQMKKTIVIRMLAAVITFFVCMFPFPHLQRLIFLYAKN-----MDNYLDINEALFSIAG 342  
QY 342 QLFLYLSASINPILYNLISKYRAAFAKLLARKS 375  
Db 343 FAYIVSVCTVNPVIVSVMSRRYR-VAFRELLCGKA 375

RESULT 4  
A88013  
protein K1084.4 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: A88013  
R.anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: A88013  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-418 <STO>  
A:Cross-references: UNIPROT:O17239; GB:chr\_II; PIDN:AB71009.1; PID:g2429475; GSPDB:GN000  
C:Genetics:  
A:Gene: K1084.4  
A:Map position: 2

Query Match 20.3%; Score 437; DB 2; Length 418;  
Best Local Similarity 30.1%; Pred. No. 1.9e-27;  
Matches 109; Conservative 78; Mismatches 137; Indels 39; Gaps 10;  
QY 29 RCSPPFLGALVPVTAVCLCLFVVGSGNVVTVMLIGRYDRMRTTNLYLGSMAVSDLL-I 87  
Db 24 RQ--SAGIVATVITYITIFLGLFGNICTIVIAANKSMHNPNTYLFSLAVSDIAL 81  
QY 88 ILGLPFDLYR-LWRSRPWVFGPCLCLSLYVGEQCTYATLLHMTALSERYLAICRPLA 146  
Db 82 ILGLPMEFYQSLDYSVPYRFBSEGIKARAFLEIFTSYASIMICCFERWLAICHPLRS 141  
QY 147 RVLVTRRRVRVLAIVLWALLSAGPFLVGVQDP-----GISVVGPLNGTARIASSPLA 203



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Db 142 KIFSLWRANVLIIIAWTISFVCAIPPIAFIVQINKLPIPEDAKYQPTWKNKVSFFAVGVLN 201
Qy 204 SSPLWLGRAPPPSPSPETAAALFSREC-----RPSAQLGALRVLMLVTTTAYFFL 258
Db 202 -----NRIPVS-----TDGIFVLHTEFCAMNQSRDQKM-----IIIFATVFFVI 244
Qy 259 PFLCLSLYGLIGRELMSRRRLRGP--AASGRGRHQTVRVLLVVLAFIICWLPFHV 316
Db 245 PAIAIVIMYAHIAVLESSEIDKGDVMVKRKNKSNRTVLKMLLSVITTFICWLPFHI 304
Qy 317 GRIIIVNTEDSRMVFQSVFNVALQLFVLS-----ASINPILYNLISKYRAAFL 369
Db 305 QLLSVYTTWSTTTISPVPQLSMIVFIYISFCYSYSAANPILYNLISQIRSAFCRT 364
Qy 370 LL 371
Db 365 IL 366

RESULT 5
JC8012
G protein-coupled, neuropeptide pyrokinin-2 receptor (CG8795) - fruit fly (Drosophila mel)
C:Species: Drosophila melanogaster
C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: JC8012
R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R.
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: JC8011; PMID: 12951076
A:Accession: JC8012
A:Molecule type: mRNA
A:Residues: 1-595 <ROS>
A:CROSS-references: GB:AY277899
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
e, feeding, and behavior.
C:Genetics:
A:Gene: CG8795
A:introns: 115/1; 170/2; 214/3; 281/1; 352/3; 390/3
A:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 19.5%; Score 420; DB 2; Length 595;
Best Local Similarity 29.7%; Pred. No. 6.4e-26;
Matches 121; Conservative 62; Mismatches 137; Indels 88; Gaps 13;

Qy 34 PLGALVPVTVAVCLCLFVGVSGNVVTVMLIGRYRDMRTTNLYLGLSMVAVSDLLILL-GLP 92
Db 58 PLSLLATLSVGVALLFIAGVLGNLTICVISNNFWHTATNFYLFNLAISDMILLCSGP 117
Qy 93 FDLYRLRSRPVFGPLICRLSLYVGECTYATLHMTALSVERYLAICRPLRARVLVTR 152
Db 118 QDLYNLHPNDNYPFSDSICILSVLSEATANATVLTITAFVRYAICHPRQHTMSKL 177
Qy 153 RRVRALIAVLAVALLSAGPFLFVGVQDPCISVVPGLNGTARTASPLASSPPLMLSR 212
Db 178 SRVAKFIFAIWTAAULLALPOAIFSV-----VMQGTGCTCKNDFFAH----- 222
Qy 213 APPSPSPGPETAEEAALFSRECRPSAQLGALRVMLVTTTAYFFL--PFLCLSLYGLI 270
Db 223 -----VFVSGFLFFGGMPTAICVLYVLI 246
Qy 271 GRELMSR--RPL-----RGAASGRGRHQTVRVLLVVLAFIICWLPFHVGRIRI- 319
Db 247 GVKLKRSRLQLALPRCYDVNRGISAQTR-----VIRMLVAVAVAFICWAPFAQRLM 300
Qy 320 -IYINTESRMMYFQYFNIVALQ---LFYLSASINPILYNLISKYRAAFAKLLAR-- 373
Db 301 AVYGSTGIESQWFDNVFSILDYTSGLVYFLSTCINPLLYNIMSKFR-EAFKVTLARHF 359
Qy 374 ----KSRPRGFHRS-----RDTAGEVAGDTGGDTVGYTETSANVTMG 412
Db 360 GLGGKNGRGLPHTYISALRRNTQSGIRLHT-TDSVRTTWTSMATTTTG 406
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RESULT 6
S68822
neurotensin receptor 2, levocabastine-sensitive - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C:Accession: S68822
R:Chalon, P.; Vita, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpach, B.; le Fur, G.;
FBBS Lett. 386, 91-94, 1996
A:Title: Molecular cloning of a levocabastine-sensitive neurotensin binding site.
A:Reference number: S68822; MUID:96228041; PMID:8647296
A:Accession: S68822
A:Molecule type: mRNA
A:Residues: 1-416 <CHA>
A:CROSS-references: UNIPROT:Q63384; GB:X97121; NID:G1483579; PIDN:CAA65787.1; PID:G14835
A:Experimental source: hypothalamus
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:33-58/Domain: transmembrane #status predicted <TM1>
F:70-91/Domain: transmembrane #status predicted <TM2>
F:110-131/Domain: transmembrane #status predicted <TM3>
F:155-175/Domain: transmembrane #status predicted <TM4>
F:204-230/Domain: transmembrane #status predicted <TM5>
F:296-315/Domain: transmembrane #status predicted <TM6>
F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 18.6%; Score 401; DB 2; Length 416;
Best Local Similarity 29.4%; Pred. No. 1.5e-24;
Matches 122; Conservative 68; Mismatches 145; Indels 80; Gaps 13;

Qy 18 PWPALP-----PCDERCSPPLGALVPVTVAVCLCLFVGVSGNVVTVMLIGRYRDMRT 71
Db 6 PWPPRPSPSAGLSLEARLGVDTRLWAKVLFATLYSLIFAFGTAGNALSVHVVVKARAGRP 65
Qy 72 -TTNLYLGSMAVSDLLILL-GLPDLVR-LWRSRPWVFGPLICRLSLYVSGCTVATLLH 128
Db 66 GLRYHVLSTLSALSALLLVSNPMELYNFVWSHPWFGDLGCRGYVFRRLCATVLS 125
Qy 129 MTALSVERYLAICRPLRARVLVTRRRALIAVLAVALLSAGPFLFVLGV----- 179
Db 126 VASLSAERCLAVCQPLRARRLTTPRTRRLSLVWVASLGLALPMVIMQKHEVASDG 185
Qy 180 EQDGIISVVPGLNGTARTIA-----SSPLASSPPLMLSRAPPPSPGPETAEEA 228
Db 186 EPEPASRVTCTVLVSRATLQVFIQVNLVSVFALPLATAFL-----NGITVNHLM 234
Qy 229 ALFSRECRPSAQLGALRVMLVTTTAYFFLCLSLYGLIGRELMSRRPLRGPAASG 288
Db 235 ALYS-QVPSAQVSSIPSRLLEUSE-----EGLGFTITWRKTLSLGVQASLV 281
Qy 289 RE-----RGRQTVRVLLVVLAFIICWLPFHVGRIRIINTED-----SRMMYFQYFNI 338
Db 282 RHKDAQSIRSLQHSQVLAIRAVVVICWLPYHARRLMYCVIPDDGTWNLVDYFHYFVM 341
Qy 339 VALQFLYLSASINPILYNLISKYRAAFAKLLARKSPRGFHRSDRTAGEVAGD 393
Db 342 VTNTLFYVSSAVTPIYNAVSSFR-----KLFL-----ESLGLSCGE 379

RESULT 7
JC8011
G protein-coupled neuropeptide pyrokinin-2 receptor (CG8784) - fruit fly (Drosophila mel)
C:Species: Drosophila melanogaster
C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: JC8011
R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, I.;
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: JC8011; PMID: 12951076
A:Accession: JC8011
A:Molecule type: mRNA
A:Residues: 1-658 <ROS>
A:CROSS-references: GB:AY277898
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
```

development, diapause, feeding, and behavior.

C;Genetics:

A;Gene: C98784

A;Introns: 160/1; 215/2; 259/3; 326/1; 400/3

C;Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 18.2%; Score 392; DB 2; Length 658;  
Best Local Similarity 30.2%; Pred. No. 1.2e-23;  
Matches 121; Conservative 55; Mismatches 121; Indels 104; Gaps 15;

QY 1 MGSPPNGSDGEGAREPPWALPPCDERRCSFPFGALVPVAVCLC---LFWVGSGNV 57

DB 83 LGST-NGTNASTMAAD-----SPVDE-----SLTRLATVCAVLIIEVAGVLGNL 126

QY 58 VTVMILGRYDRMTTNLYLGSMAVSDLLIL-GLPDFLYRLWRSRPWVFGPLLCLRLSLY 116

DB 127 ICIVISRNFMHTATNFYLFNLAVSDLLILVSGIPQELYNLYWYDMYFFTDAMCIMGSV 186

QY 117 VGEQCTYATLLHMTALSVRYLAICRPLARVLVTRRRVRLALVAVALLSAGP--FL 174

DB 187 LSEMAANATVLTITFTVRYTAICHPPTHQTKSLRAIKFIFAILAAAPLLALPQAMQ 246

QY 175 FLVGEODGIGSVVGLNGTARIASSPLASSPPLWLSRAPPSGPGTAAALFSRE 234

DB 247 FSV-VYQNEGYCTWENDFYAHV----- 268

QY 235 CRPSPAQLGALRWLVVTTAYPFL--PFLCLSLYLGLIGLELWSSR-----RPLR 282

DB 269 -----FVSGPIFFGPGMTAICVLVLIGVKLRRLQLSLPRRTFDNR 313

QY 283 GPAASGRGRHRTQTVRLVAVVLAFLICLWPLPHVGRIL-----YINTEDSRMYFSQYF 336

DB 314 GLNAQR-----VIRMLVAVAVAPFLCWAPFHAQRLMAVYGLNLINIGISRDA-FNDYF 366

QY 337 NIVALQ---LFLVLSASINPILYLSKKYRAAFKLLARK 374

DB 367 RILDYTSGLVYFLSTCINPLLYNIMSHKFR-EAFKITLTRQ 406

RESULT 8

T15816

hypothetical protein C48C5.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T15816

R;Pavello, A.

A;Description: The sequence of C. elegans cosmid C48C5.

A;Reference number: Z18410

A;Accession: T15816

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-378 <PAV>

A;Cross-references: UNIPROT:Q18701; EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB370

A;Experimental source: strain Bristol N2; clone C48C5

C;Genetics:

A;Gene: CESP:C48C5.1

A;Map position: X

A;Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1

C;Superfamily: adenosine receptor A1

Query Match 17.4%; Score 375; DB 2; Length 378;  
Best Local Similarity 28.7%; Pred. No. 1.6e-22;  
Matches 97; Conservative 70; Mismatches 135; Indels 36; Gaps 9;

QY 38 LVPVAVCLCLFVVGSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLIL-LGLPDFLY 96

DB 51 LYKXTALYIFILVGVIGNTTCLVKKHPMMKTHASMYLNLAVSDILVLCVGLPFV 110

QY 97 RLWRSRPWVFGPLLCLRLSLYGEQCTYATLLHMTALSVRYLAICRPL-RAVVLTRRV 155

DB 111 MNWQYPPWPPDYICNLKALIAETSSVSILTILFAERYVAVCHPLFLMKVQPFKNI 170

QY 156 RALIAVLMAVALLSAGPFLVGVQDPGIGSVVPLNGTARIASSPLASSPPLMLSRAPP 215

DB 171 GTIIGFTWIFSLCAMP--FAIHRADYIMKSWFGTONRIPVKSQKCM----- 217

QY 216 PSPSPGPETAALAFSRECRPSPAQLGALRWML-WVTTAYFPLFLCLSLYLIGLIGREL 274

DB 218 -----IAVMF-----EPKLASTFKILFHSAIAFFALFLFTIVLYARIACKV 260

QY 275 WSSRRLRGPASGRGRHRTQTVRLVAVVLAFLICLWPLPHVGRILYINTEDSRMW-YFS 333

DB 261 -SSNRTIQPGELDTEELQMRINALCAVSAFFICYLPFQQLRLLFPYFDFNEVILTWN 319

QY 334 QYFNIVALQLFYLGSASINPILYLSKKYRAAFKLLL 371

DB 320 QYMFISGLFYLATIINPIAYNLASSRFR-RAFKDIL 356

RESULT 9

I57940

somatostatin receptor 5 - rat

N;Alternate names: somatotropin release-inhibiting factor subtype 28 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

A;Accession: I57940; I57949; S39244

R;O'Carroll, A.M.; Lolait, S.J.; Koniig, M.; Mahan, L.C.

Mol. Pharmacol. 42, 939-946, 1992

A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref

A;Reference number: I57940; MUID:93125499; PMID:1362243

A;Accession: I57940

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-363 <OCAL>

A;Cross-references: UNIPROT:P30938; GB:L04535; NID:g409238; PIDN:AAAL7029.1; PID:g409233

R;O'Carroll, A.M.; Lolait, S.J.; Koniig, M.; Mahan, L.C.

Mol. Pharmacol. 44, 1278, 1993

A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref

A;Reference number: I57949; MUID:94088493; PMID:8264565

A;Accession: I57949

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 341-363 <OCA2>

A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948

A;Experimental source: pituitary

R;Penetta, R.; Greenwood, M.; Patel, Y.C.

submitted to the EMBL Data Library, August 1993

A;Description: Correction of the nucleotide and amino acid sequence of the rat somatosta

A;Reference number: S39244

A;Accession: S39244

A;Molecule type: mRNA

A;Residues: 309-363 <PEN>

A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912

C;Genetics:

A;Gene: SSTR5

C;Superfamily: vertebrate rhodopsin

Query Match 16.7%; Score 359; DB 2; Length 363;  
Best Local Similarity 27.3%; Pred. No. 2.9e-21;  
Matches 110; Conservative 60; Mismatches 149; Indels 84; Gaps 12;

QY 5 WNGSDGEGAREPPWALPPCDERRCSFPFLGA---LVPVAVCLCLFVVGSGNVTVTM 61

DB 12 WNASAASSGNHN--WSLVG-----SASPMGARAVLPVLYLVC--TVGLSGNTLVIY 60

QY 62 LIGRYDRMTTNLYLGSMAVSDLLILGLPDFLYRLWRSRPWVFGPLLCLRLSLYVGE 121

DB 61 VVLRHAKKTVTVTIINLAVADVFLMLGLPFLATQNAVVSWFPGFLCLKLVMLDGIN 120

QY 122 TYATLLHMTALSVRYLAICRPLARVLVTRRRVRLALVAVALLSAGPFLFLVGVEQ 181

DB 121 QFTSIFCLMWSDVRLAVVHPLRSARWRPRVAKMASAAVWVFLSLMSLPLLVFADVQE 180

QY 182 DPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSGPGTAAALFSRECRPSPAQ 241

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Db 181 G-----WGTCLNS-----W-----PEPVG 194
QY 242 LGALRMLVMTTAYFPFLPCLISILYGLI-----GRELWSSRRPLRGPAASGRGRHR 294
Db 195 LWGAFAITVTSVLGFFGPLLVLICLCVLLIWKVAAGMRVGSRR-----RRRSEP 244
QY 295 QTVRVLLVVVLAFLICWLPFHVGRIIYN-TEDSRMMYFSQYFNIVALQLFLYLSASINPI 353
Db 245 KVRMMVVVVVLFVGCWLPFFIVNTLVNLAFTLPEBFTSAGLYFFVVVLS--YANSCANPL 302
QY 354 LYNLISKYRAAAAFKLLARKSRPGFHRSDRTAGEVAGDTGG 396
Db 303 LYGLSDNFRQSRFKVLCLR-----ROYGMEDADAIEPRPDKSG 341

RESULT 10
A46226
somatostatin receptor 3 - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46226; S32501
R:Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Seino, M.; Endocrinol. 6, 2136-2142, 1992
A:Title: Somatostatin receptors, an expanding gene family: cloning and functional characterization
A:Reference number: A46226; MUID:93149123; PMID:1337145
A:Accession: A46226
A:Molecule type: DNA
A:Residues: 1-418 <YAM>
A:Cross-references: UNIPROT:P32745; GB:M96738; NID:G338498; PID:AAA60592.1; PID:G338499
A>Note: sequence extracted from NCBI backbone (NCBI:123685, NCBI:P123690)
R:Corneess, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent, G.; FEBS Lett. 321, 279-284, 1993
A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays preference
A:Reference number: S32501; MUID:93238970; PMID:8097479
A:Accession: S32501
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <COR>
C:Genetics:
A:Gene: GDB:SSTR3
A:Cross-references: GDB:134187; OMIM:182453
A:Map position: 22q13.1-22q13.1
A:Introns: status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:81-106/Domain: transmembrane #status predicted <TM1>
F:118-139/Domain: transmembrane #status predicted <TM2>
F:159-181/Domain: transmembrane #status predicted <TM3>
F:203-233/Domain: transmembrane #status predicted <TM4>
F:255-282/Domain: transmembrane #status predicted <TM5>
F:289-316/Domain: transmembrane #status predicted <TM6>
F:17-30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:116-191/Disulfide bonds: #status predicted
F:151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:251/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
F:256/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predicted
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 16.6%; Score 357.5; DB 2; Length 418;
Best Local Similarity 26.9%; Pred. No. 4.5e-21;
Matches 101; Conservative 63; Mismatches 146; Indels 65; Gaps 10;
QY 11 PEGAREPPWALPPCDERRCSPPFL-----GALVPVTAIVCLCFVVGSGNVVTVMLIGR 65
Db 15 PENA-SSAWPPDATTGNVAGSPAGLAVSGVLIIFVLVVC--VGLLGNLSLVIVVR 71
QY 66 YRDMRTTNLYLGSMAVSDLLILGLPDLXLMRSRPVWFGPLLCRLSLYVGECCYAT 125
Db 72 HTAPSVTVNYILNALADELFMLGLPF-LAAQNALSYWPFGLSLMCLVMAVDGINQFTS 130
QY 126 LLMHTALSVERYLAICRPLARVLVTRRRVRLIAVLNAVALLSAGPFLVGVGEQDGI 185
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Db 131 IFCLTMSVDYRLAVVHPTRSGARWRTAPVARTVSAANVWASAVVVLVVFVSGV----- 184
QY 186 SWFGLNGTARIASSPLASSPPLMLSRAPPSPSPGPETAABAAALFSRECR---PSPAQL 242
Db 185 -----PRGMST-----CHMQWPEPAAA 201
QY 243 GALRVMLVMTTAYFPFLPCLISILYGLIGRELWSSRRPLRGPAASGRGRGRHQTQTVRVLLV 302
Db 202 WRAGFIITYTAALGFGPLLVLICLCVLLIWKVRSAGRRVWAPSCQRRRSRRRVTRMVVA 261
QY 303 VYLAFLICWLPFHVGRIIYINTE-DSRMMYFSQYFNIVALQLFLYLSASINPILYNLSK 361
Db 262 VVALFVLCWMPFYVLNVIVNVCPLPEEPAFFGLYFLVVALP--YANSCANPILYGLSYR 319
QY 362 YRAAFAKLLARKSR 376
Db 320 FK-QGFRVLLRPSR 333

RESULT 11
I57955
somatostatin receptor - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I57955
R:Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchyshyn, L.L.; Day, R.; Niznik, H.B.; Mol. Pharmacol. 45, 417-427, 1994
A:Title: Molecular cloning, functional characterization, and chromosomal localization of
A:Reference number: I57955; MUID:94195267; PMID:7908405
A:Accession: I57955
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-363 <RES>
A:Cross-references: UNIPROT:P35346; GB:L14865; NID:G431094; PID:AAA20828.1; PID:G431095
C:Genetics:
A:Gene: GDB:SST
A:Cross-references: GDB:119604; OMIM:182450
A:Map position: 3q28-3q28
C:Superfamily: vertebrate rhodopsin

Query Match 16.0%; Score 344; DB 2; Length 363;
Best Local Similarity 27.7%; Pred. No. 4.6e-20;
Matches 106; Conservative 58; Mismatches 131; Indels 88; Gaps 14;
QY 14 AREPPWALPP-----CDERR-CSPPF-LGA---LVPVTAIVCLCFVVGSGNVVTVML 62
Db 7 ASTPSWNASFGAASGGGDNRTLVGPAPSAGARAVLVPVLLVC--AAGLGNTLVIVV 64
QY 63 IGRYDRMTTNLYLGSMAVSDLLILGLPDLXLMRSRPVWFGPLLCRLSLYVGECC 122
Db 65 VLRPAKMTVTNVIYILNLAVALVYMLGLPF-LATQNAASFVWPFGLVCLVMTLDGVNQ 123
QY 123 YATLLHTALSVERYLAICRPLARVLVTRRRVRLIAVLNAVALLSAGPFLVGVGEQD 182
Db 124 FTSVFLTVMSVDYRLAVVHPTRSGARWRTAPVARTVSAANVWASAVVVLVVFVSGV 182
QY 183 PGISVVPGLNGTARIASSPLASSPPLMLSRAPPSPSPGPETAABAAALFSRECRSPAQL 242
Db 183 -----GTCNAS-----W-----PEPVCL 196
QY 243 GALRVMLVMTTAYFPFLPCLISILYGLIGRELWSSRRPLRGPAASG-----REGRHQT 296
Db 197 WGAFFIITYTAALGFGPLLVLICLCVLLIWKV-----RAAGRVGCVRRRSRKV 246
QY 297 VRVLLVVLAFIICWLPFHVGRIIYI-----NTEDSRMMYFSQYFNIVALQLFLYLSASIN 351
Db 247 TRMLVVLVVLVAGCWLPEFTVNI VNLVALVQEPASAGLYF---FWVI---LSYANSCAN 300
QY 352 PILYNLISKYRAAAAFKLLARK 374
Db 301 PVLYGLSDNFRQSRFKVLCLRK 323
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A;Reference number: A48789; MUID:94052210; PMID:8234341  
A;Accession: A48789  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-380 <RES>  
A;Cross-references: EMBL:U00442; NID:g403486; PIDN:AAA18261.1; PID:g403487  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.7%; Score 339; DB 2; Length 380;  
Best Local Similarity 25.5%; Pred. No. 1.2e-19;  
Matches 103; Conservative 75; Mismatches 146; Indels 80; Gaps 13;

QY 6 NGS DGP EGAREPP---WPALPPCDERRCSFPFGLGALVPVTAVCLCLFVWGSGNVVTVML 62  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
DB 39 NGS VSG SEDQLEPAHISPAIP-----VITAVTVSVFVGVGLGNSLVNFV 83  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
QY 63 IGRYDRMTTNYLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPPLCLRLSLYVSGEGT 122  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
DB 84 IIRYTKMTATNIYIFNLALADALVTTMTFQ--SAVYLMNSWPFQDLVKIVISIDYNN 142  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
QY 123 YATLLHMTALSERYIAICPLBARVLVTRRRVRVALIAVLWAVALLSAGPFLFLVGVEQD 182  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
DB 143 FTSIFTLTMSVDRYTAVCHPVKALDFTPLKAKIINICIIWLLASSVGISAIVLGGTKVR 202  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
QY 183 PGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGETAEMAAALFSRECPSPAQL 242  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
DB 203 EDVDVIE-----CSLQFPDDEYSWMD-----LFMKIC----- 229  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
QY 243 GALLRVLMTVTTAYFFLPFLCLSLYLGLIGRELWSSRRPLRGPAASGRGRHROTIVLLV 302  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
DB 230 -----VFVFAFVPLVLIIVCYTILMURL-KSVLLSG--SREKORNLRIITKVLV 278  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
QY 303 VILAFTICMLPFHVGRIIYI--NTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
DB 279 VVAFFIICWTHIFILVEALGSTSHSTAVLSSVYF--CIALGYTNSSLNPVLYAFLDE 335  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
QY 361 KYRAA-----APKLLARKSRPGFRHSRDTAGEVAG--DTGG 396  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
DB 336 NFKRCFRDFFCPIKMEROST-----NRVNTVODPASMRDVG 375  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

Search completed: April 11, 2005, 21:05:35  
Job time : 19.5539 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:44:49 ; Search time 742.96 Seconds  
(without alignments)  
11075.206 Million cell updates/sec

Title: US-09-719-485-4

Perfect score: 1390

Sequence: 1 atgggcgcgccttggaacgg.....acgtgaagacatggggataa 1390

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1390	100.0	1390	3	Aaz45404 cDNA enco
2	1161	83.5	1161	4	Aaf83684 Short for
3	1161	83.5	1161	12	Adn11762 Human mot
4	1078	77.6	1239	3	Aaz45403 cDNA enco
5	1078	77.6	1239	4	Aaf85449 Nucleotid
6	1078	77.6	1239	4	Aaf83683 Long form
7	1078	77.6	1239	6	Abk90132 DNA enco
8	1078	77.6	1239	8	Abz42842 Human mot
9	1078	77.6	1239	12	Adn11760 Human GPC
10	1078	77.6	1239	12	Ado30072 Human GPC
11	1078	77.6	1239	12	Adq37920 Human G-p
12	1078	77.6	1506	4	Aai65989 Human GPR
13	1052	75.7	110000	10	Adg70447 Human ANG
14	1052	75.7	110000	10	Abz79565 CLD8 and
15	1047.2	75.3	2040	3	Aaa46116 Human G p
16	1047.2	75.3	2040	12	Adg86490 Human hGP
17	1047.2	75.3	2040	12	Adp20283 Human GPC
18	1040.8	74.9	2040	12	Adg86512 Human orp
19	1038	74.7	3066	3	Aaz45402 Genomic s
20	754.6	54.3	1203	4	Aaf85448 Nucleotid

21	546	39.3	813	4	Aaf85447 Nucleotid
22	501.2	36.1	1179	6	Abq47146 Oligonucl
23	501.2	36.1	1179	6	Abq47147 Oligonucl
24	437.2	31.5	1179	6	Abq47149 Oligonucl
25	437.2	31.5	1179	6	Abq47148 Oligonucl
26	283	20.4	283	2	Aav28290 Galanin r
27	283	20.4	283	2	Aav32851 Galanin r
28	283	20.4	283	2	Aav44930 Galanin r
29	283	20.4	283	6	Abk14060 Rat galan
30	248.2	17.9	1050	3	Aaz61492 cDNA enco
31	234.8	16.9	1063	2	Aat69754 Swine gro
32	234.8	16.9	1063	2	Aat68662 Pig growt
33	233.2	16.8	1029	2	Aat69755 Swine gro
34	233.2	16.8	1029	2	Aat68663 Pig growt
35	231.6	16.7	1095	3	Aaz45993 cDNA enco
36	231.6	16.7	4009	3	Aaz45967 DNA enco
37	230	16.5	1092	12	Ado29027 Mouse nov
38	229	16.5	250	10	Acas5761 Pig signa
39	229	16.5	250	12	Adi55557 Human pol
40	228.8	16.5	870	8	Abz42674 Human gro
41	228.8	16.5	1122	2	Aat68665 Human gro
42	228.4	16.4	1092	4	AAH27800 Rat growt
43	228.4	16.4	3129	2	Aat69759 Rat growt
44	228.4	16.4	3129	2	Aat68667 Rat growt
45	227.8	16.4	1088	2	Aat69756 Human gro

#### ALIGNMENTS

##### RESULT 1

AAZ45404

ID AAZ45404 standard; cDNA; 1390 BP.

XX AAZ45404;

AC AAZ45404;

DT 27-MAR-2000 (first entry)

XX cDNA encoding the motilin receptor splice variant MTL-R1b.

XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;

KW spliced form; MTL-R1a; MTL-R1b; gastric motility disorder;

KW functional defect; neurological disorder; scleroderma; colonoscopy;

KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;

KW infection; stress-related motility disorder; psychogenic disorder;

KW gastroparesis; gastro-oesophageal reflux disease; constipation;

KW chronic idiopathic pseudo obstruction; acute faecal impaction;

KW postoperative ileus; gallstones; infantile colic; diarrhoea;

KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;

KW endoscopy; duodenal intubation; ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1161

FT /\*tag= a

FT /product= "MTL-R1b"

XX WO9964436-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012773.

XX 12-JUN-1998; 98US-0089098P.

XX (MERI ) MERCK & CO INC.

XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;

XX Pong S, Smith RG;

XX WPI; 2000-105868/09.

XX P-ESDB; AAY54146.

XX Novel receptor protein for screening compounds used in treating irritable  
PT bowel syndrome, constipation and other gastric conditions.  
XX Claim 6; Fig 4; 44pp; English.  
XX The present sequence encodes splice variant MTL-R1B of the motilin  
CC receptor. The gene encodes a G-protein coupled receptor, and is  
CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A  
CC (see AY54145) and MTL-R1B (see AY54146). MTL-R1A is a functional seven  
CC transmembrane domain form, and MTL-R1B is a truncated five transmembrane  
CC domain. The MTL-R1 proteins are used to identify agonists and antagonists  
CC which can be used for treating gastric motility disorders, functional  
CC defects, disorders secondary to neurological disorders e.g. scleroderma,  
CC paraneoplastic syndromes radiation induced dysmotility, diabetes,  
CC infections, stress-related motility disorders, psychogenic disorders,  
CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic  
CC idiopathic pseudo obstruction, acute faecal impaction, postoperative  
CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer  
CC dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used  
CC in the preparation for colonoscopy, endoscopy and duodenal intubation  
XX  
SQ Sequence 1390 BP; 190 A; 496 C; 436 G; 268 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1390; DB 3; Length 1390;  
Best Local Similarity 100.0%; Pred. No. 4.9e-241;  
Matches 1390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGGACGCCCCGTGAAGCGGACGAGCGGCCCCCGAGGGGGCGCGGGAGCCGCGTGGCCC 60  
DB 1 ATGGGACGCCCCGTGAAGCGGACGAGCGGCCCCCGAGGGGGCGCGGGAGCCGCGTGGCCC 60  
QY 61 GCGCTGCGGCTTGGGACGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGTGTGGCG 120  
DB 61 GCGCTGCGGCTTGGGACGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGTGTGGCG 120  
QY 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
DB 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
QY 181 ATGCTGATCGGGCGGTACCGGACATGCGGACACACCACTTGTACTGGGACGATG 240  
DB 181 ATGCTGATCGGGCGGTACCGGACATGCGGACACACCACTTGTACTGGGACGATG 240  
QY 241 GCGGTGCGGACCTACTCATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 300  
DB 241 GCGGTGCGGACCTACTCATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 300  
QY 301 TCGGCGCCCTGGGTGTGCTGCGGCGCTGTGCTGCGGCTGTGCTGCTGCTGCTGCTGCTG 360  
DB 301 TCGGCGCCCTGGGTGTGCTGCGGCGCTGTGCTGCGGCTGTGCTGCTGCTGCTGCTGCTG 360  
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DB 361 TGCACCTAGCCACGCTGTGACATGACCGGCTCAGCGTTCAGCGGTACCTGCGCATC 420  
QY 421 TGCAGCGCGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 421 TGCAGCGCGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 GTGCTGTGGGCGTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
DB 481 GTGCTGTGGGCGTGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
QY 541 CAGGACCGGCGATCCGTAAGTCCCGGCGCTCAATGGACCGCGGATCCGCTCCG 600  
DB 541 CAGGACCGGCGATCCGTAAGTCCCGGCGCTCAATGGACCGCGGATCCGCTCCG 600  
QY 601 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
DB 601 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
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661 GGGCCCCGAGACCGCGGAGCGCGGCGTGTTCAGCCCGGAATGCCGGCGAGCCCGCG 720  
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721 CAGTGGGCGCGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
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781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGAGGAGCGAGCGCGGCGCG 840  
841 CTGGAGCGCGCGCGCTGCGGGGAGAGAGGCGCACCGGAGAGCGGCTGCGGCGTCTG 900  
841 CTGGAGCGCGCGCGCTGCGGGGAGAGAGGCGCACCGGAGAGCGGCTGCGGCGTCTG 900  
901 CGTAAGTGGAGCGCGCTGCTTCCAAAGAGCGCTGCTGAGTCCGCGCGCGCGGAGCC 960  
901 CGTAAGTGGAGCGCGCTGCTTCCAAAGAGCGCTGCTGAGTCCGCGCGCGCGGAGCC 960  
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961 GCGCAAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1020  
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1081 CTGGTTCGCTTCCAGCTTGGCAGATCATTTACATAAAACACGGAAGATTTCGCGGATGAT 1140  
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1141 GTACTTCTCTCAGTACTTTAAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
1141 GTACTTCTCTCAGTACTTTAAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
1201 CAACCCATCTCTACACCTTCAAGAGTACAGAGGAGTACAGAGGAGTTCGCGGAGT 1260  
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1261 GCTCGAAGGAGTCCAGGCGGAGAGGCTTCCACAGAGGAGGAGGAGTTCGCGGAGT 1320  
1261 GCTCGAAGGAGTCCAGGCGGAGAGGCTTCCACAGAGGAGGAGGAGTTCGCGGAGT 1320  
1321 TGCAGGAGGAGTCCAGGAGGAGTACAGGAGGAGTACAGGAGGAGTTCGCGGAGT 1380  
1321 TGCAGGAGGAGTCCAGGAGGAGTACAGGAGGAGTACAGGAGGAGTTCGCGGAGT 1380  
1381 GATGGGATAA 1390  
1381 GATGGGATAA 1390

RESULT 2  
AAP83684  
ID AAP83684 standard; DNA; 1161 BP.  
XX  
AC AAP83684;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Short form of motilin receptor, GPR-38B isoform encoding DNA.  
XX  
KW zsig33; signal transduction; hormone; enzyme; neural development;  
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
KW insulin-like growth factor-1; growth hormone; bone; gastrointestinal;  
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R; ds;  
KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38B; isoform.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
1..1161  
/\*tag= a



FT XX /product= "GPR-38B"  
 PN WO200138355-A2.  
 XX 31-MAY-2001.  
 XX 22-NOV-2000; 2000WO-US032074.  
 XX 22-NOV-1999; 99US-0166765P.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;  
 XX WPI; 2001-355879/37.  
 DR P-PSDB; AAB62653.  
 DR  
 XX Forming reversible peptide receptor complex for purifying cell and  
 XX peptides, stimulating signal transduction and modulating hormone  
 PT secretion, involves contacting a receptor with zsig33 polypeptide.  
 FT  
 XX Disclosure; Page 106-109; 111pp; English.  
 XX  
 CC The invention relates to a method of forming a reversible peptide-  
 CC receptor complex that involves providing an immobilized receptor, and  
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37  
 CC of AAB62649), where the receptor binds to the zsig33 peptide. The method  
 CC is useful for purifying cells, purifying a peptide, stimulating signal  
 CC transduction in a cell expressing a receptor. It is also useful for  
 CC modulating secretion of hormones, neural development and/or utilization,  
 CC gastric contractility, nutrient uptake, secretion of digestive and  
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor  
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth  
 CC hormone secretion in a mammal having a disease associated with abnormal  
 CC levels of growth hormone, such as osteoporosis, bone repair, bone  
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,  
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,  
 CC protein catabolic responses after surgery, cachexia, protein loss,  
 CC dwarfism, wound healing and ovulation induction, treating a mammal having  
 CC a metabolic disorder requiring neurological feedback, such as satiety  
 CC regulation, glucose absorption and metabolism and neuropathy-associated  
 CC gastrointestinal disorders, and stimulating glucose-induced insulin  
 CC release in a mammal. The present sequence represents the DNA encoding the  
 CC short form of motilin receptor, GPR-38B (one of the two isoforms of GPR38  
 CC which result from alternative splicing). GPR38 has homology to the human  
 CC G-protein coupled receptor, GHS-R  
 XX  
 SQ Sequence 1161 BP; 126 A; 436 C; 372 G; 227 T; 0 U; 0 Other;  
 Query Match 83.5%; Score 1161; DB 4; Length 1161;  
 Best Local Similarity 100.0%; Pred. No. 8e-200;  
 Matches 1161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGAGCCCTGGAACGAGGAGACGGCCCCGAGGGGGCGCGGAGCCCGCTGGCCCC 60  
 Db 1 ATGGGAGCCCTGGAACGAGGAGACGGCCCCGAGGGGGCGCGGAGCCCGCTGGCCCC 60  
 Qy 61 GCGGTGCGCGCTGCGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGGTGGCG 120  
 Db 61 GCGGTGCGCGCTTGGGAGCGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGGTGGCG 120  
 Qy 121 GTGACCGCTGTGTGCTGTGCTGTGTTCTGCTGCGGGGTGAGCGGCAACGCTGGTACCGGTG 180  
 Db 121 GTGACCGCTGTGTGCTGTGCTGTGTTCTGCTGCGGGGTGAGCGGCAACGCTGGTACCGGTG 180  
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 Db 181 ATGCTGATCGGGCGCTACCGGACATGCGGACCAACCACTTGTACTCGGCGAGCATG 240  
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 Db 241 GCCGTGTCGACCTACTCATCTGCTCGGGCTGCGGCTTGCACCTGTACCGGCTCTGGGCG 300

Qy 301 TCGGGCCCTGGGTGTTGGGCGCGTGTCTGCGCGCGCTGCTCCCTTACGTGGGCGAGGGC 360  
 Db 301 TCGGGCCCTGGGTGTTGGGCGCGTGTCTGCGCGCGCTGCTCCCTTACGTGGGCGAGGGC 360  
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 Db 361 TGCACCTAGCGCAGCTGTGCACATGACCGCGCTCAGCGTGCAGCGCTACTCTGGCCATC 420  
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 Qy 721 CAGTGGGCGCGCTGCTGCTCATCTGTGGGTACACCGCGCTACTTCTCTGCGCCCTT 780  
 Db 721 CAGTGGGCGCGCTGCTGCTCATCTGTGGGTACACCGCGCTACTTCTCTGCGCCCTT 780  
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 Qy 901 CGTAAGTGGAGCGCGCTGTTCCAAAGACGCTGCTGAGTCCGCGCGCGCGCGGAGCC 960  
 Db 901 CGTAAGTGGAGCGCGCTGTTCCAAAGACGCTGCTGAGTCCGCGCGCGCGCGGAGCC 960  
 Qy 961 GCGCAACGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 Db 961 GCGCAACGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 Qy 1021 TTTCTATTTGATTCAGGCTCCAGCGCTCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 Db 1021 TTTCTATTTGATTCAGGCTCCAGCGCTCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 Qy 1081 CTGCTTGGCTTCCAGCTTGGCAGATTCATTAACACGAGAGTTCGCGGATCAT 1140  
 Db 1081 CTGCTTGGCTTCCAGCTTGGCAGATTCATTAACACGAGAGTTCGCGGATCAT 1140  
 Qy 1141 GTACTTCTCTCAGTACTTTAA 1161  
 Db 1141 GTACTTCTCTCAGTACTTTAA 1161

RESULT 3  
 ADN11762  
 ID ADN11762 standard; cDNA; 1161 BP.  
 XX  
 AC ADN11762;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human motilin receptor GPR-38B coding sequence.  
 XX ss; gene; human; zsig33; body weight; body mass; antibody; antagonist;  
 KW gastrointestinal; antiinflammatory; antiulcer; vulnerary;

KW growth hormone secretagogue; GHS-R; peptide-antibody complex;  
 XX motilin receptor.

OS Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 1..1161

FT /\*tag= a  
 FT /product= "motilin receptor GPR-38B"

XX WO2004033645-A2.

XX PN 22-APR-2004.

XX PF 06-OCT-2003; 2003WO-US031804.

XX PR 07-OCT-2002; 2002US-0416918P.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Jaspers SR, Shepard PO, Bishop PD, Kuijper JL, Deisher TA;

XX WPI; 2004-340913/31.

XX DR P-PSDB; ADN11763.

XX Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,  
 PT inhibiting signal transduction in a cell expressing a growth hormone  
 PT secretagogue receptor, or treating a metabolic disorder.

XX PS Disclosure; Page 96-98; 100pp; English.

XX The present invention relates to the use of a zsig33 peptide for forming  
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal  
 CC transduction in a cell expressing a growth hormone secretagogue receptor  
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite  
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a  
 CC mammal, or treating a metabolic disorder. The peptide is useful for  
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting  
 CC signal transduction in a cell expressing a GHS-R, decreasing fat  
 CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting  
 CC growth hormone secretion in pituitary cells of a mammal, or treating a  
 CC metabolic disorder. The zsig33 polypeptides can be used to study  
 CC proliferation or differentiation in stomach, lung, pituitary,  
 CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,  
 CC skeletal muscle or pancreas. They are also useful in delivering  
 CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are  
 CC also useful for promoting wound healing. The polypeptides, nucleic acids  
 CC and antibodies are useful for diagnosing, treating or preventing  
 CC disorders associated with gastric reflux, gastroparesis, modulation of  
 CC secretion of pituitary hormones, including growth hormone, Crohn's  
 CC disease, metabolic wasting, gastric ulcers, weight management, or  
 CC degenerative disease. The present sequence is the human motilin receptor  
 CC GPR38B coding sequence shown in the exemplification of the invention.

XX SQ Sequence 1161 BP; 126 A; 436 C; 372 G; 227 T; 0 U; 0 Other;

Query Match 83 5%; Score 1161; DB 12; Length 1161;  
 Best Local Similarity 100.0%; Pred. No. 8e-200;  
 Matches 1161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGGCAGCCCTTGAACGGCAGCAGCGCCCGAGGGGGCGCGGAGCCCGTGGGCC 60  
 DB 1 ATGGCAGCCCTTGAACGGCAGCAGCGCCCGAGGGGGCGCGGAGCCCGTGGGCC 60  
 QY 61 GCGCTGCGCCCTTGGCAGAGCGCGCTGCTGCCCTTTCCCTGGGGCGCTGGTGGCG 120  
 DB 61 GCGCTGCGCCCTTGGCAGAGCGCGCTGCTGCCCTTTCCCTGGGGCGCTGGTGGCG 120  
 QY 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 DB 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 QY 181 ATGCTGATCGGGCGGTACCGGACATGCGGACCAACCAACTTGTACTTGGGCGCATG 240

DB 181 ATGCTGATCGGGCGGTACCGGACATGCGGACCAACCAACTTGTACTTGGGCGCATG 240  
 QY 241 GCGGTGTCGACCTACTCATCTGCTGGGCTGCGGTTCGACCTGTATCCGCTCTGGGCG 300  
 DB 241 GCGGTGTCGACCTACTCATCTGCTGGGCTGCGGTTCGACCTGTATCCGCTCTGGGCG 300  
 QY 301 TCGGGCCCTTGGGTTCGGGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCG 360  
 DB 301 TCGGGCCCTTGGGTTCGGGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCG 360  
 QY 361 TGCACCTACGCGCAGCTGCTGCACATGACCCGCTCAGCGTCGAGCGCTACTTGGCCATC 420  
 DB 361 TGCACCTACGCGCAGCTGCTGCACATGACCCGCTCAGCGTCGAGCGCTACTTGGCCATC 420  
 QY 421 TCGCGCCGCTTCCGCGCCCGCTGCTGCTGTCACCGGCGCGCTGCTGCTGCTGCTGCTG 480  
 DB 421 TCGCGCCGCTTCCGCGCCCGCTGCTGCTGTCACCGGCGCGCTGCTGCTGCTGCTGCTG 480  
 QY 481 GTGCTCTGGGCGGTGGGCGCTGCTCTGCGCGCTCCCTTCTGTTCTGCTGGGCGTCCGAG 540  
 DB 481 GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGCTCCCTTCTGTTCTGCTGGGCGTCCGAG 540  
 QY 541 CAGGACCCCGGCATCTCCGTAGTCCCGGCGCTCAATGSCACCGCGCGGATCGCTCTCTCG 600  
 DB 541 CAGGACCCCGGCATCTCCGTAGTCCCGGCGCTCAATGSCACCGCGCGGATCGCTCTCTCG 600  
 QY 601 CCTCTGCGCTGCTGCGCGCTCTCTGCTGCGGGGGCGCACCGCGCTGCTGCGGCGCTG 660  
 DB 601 CCTCTGCGCTGCTGCGCGCTCTCTGCTGCGGGGGCGCACCGCGCTGCTGCGGCGCTG 660  
 QY 661 GGGCCGAGACCGCGGAGCGCGCTGCTTACGCGCGAATGCGCGCGGAGCGCGCGCG 720  
 DB 661 GGGCCGAGACCGCGGAGCGCGCTGCTTACGCGCGAATGCGCGCGGAGCGCGCGCG 720  
 QY 721 CAGCTGGGCGCGCTGCGGTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 DB 721 CAGCTGGGCGCGCTGCGGTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 QY 781 CTGTGCTCAGCATCTCTACGGCTCATCGGGGGAGCTGTGGAGCAGCGGGGCGG 840  
 DB 781 CTGTGCTCAGCATCTCTACGGCTCATCGGGGGAGCTGTGGAGCAGCGGGGCGG 840  
 QY 841 CTGCGAGCCCGCGCGCTCGGGGGGAGAGAGCCACCGCGAGACCGCTCGCGCTCTG 900  
 DB 841 CTGCGAGCCCGCGCGCTCGGGGGGAGAGAGCCACCGCGAGACCGCTCGCGCTCTG 900  
 QY 901 CGTAAGTGAGCCCGCGGTGCTTCAAGAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 DB 901 CGTAAGTGAGCCCGCGGTGCTTCAAGAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 QY 961 GCGCAACGCTGGGTTCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB 961 GCGCAACGCTGGGTTCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1021 TTTCTATTTCGATTTCAGCTTCAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 DB 1021 TTTCTATTTCGATTTCAGCTTCAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 QY 1081 CTGTTGCTTCCAGCTTGGCAGATCATTTATATAACAGGAGATTTCGCGATGAT 1140  
 DB 1081 CTGTTGCTTCCAGCTTGGCAGATCATTTATATAACAGGAGATTTCGCGATGAT 1140  
 QY 1141 GTACTTCTCTCAGTACTTTAA 1161  
 DB 1141 GTACTTCTCTCAGTACTTTAA 1161

RESULT 4  
 AAZ45403  
 ID AAZ45403 standard; cDNA; 1239 BP.  
 XX  
 AC AAZ45403;



QY 1201 CAACCCATCTCTACACCTCATTTCAAAGAGTACAGAGCGGCGCTTTAAACTGCT 1260  
 DB 1050 CAACCCATCTCTACACCTCATTTCAAAGAGTACAGAGCGGCGCTTTAAACTGCT 1109  
 QY 1261 GCTGCAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAAGAGGACACTGCGGGGAAGT 1320  
 DB 1110 GCTGCAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAAGAGGACACTGCGGGGAAGT 1169  
 QY 1321 TGCAGGGACACTGAGAGAGACACGGTGGGCTACCCAGAGCAAGCGCTAACGTGAGAC 1380  
 DB 1170 TGCAGGGACACTGAGAGAGACACGGTGGGCTACCCAGAGCAAGCGCTAACGTGAGAC 1229  
 QY 1381 GATGGGATAA 1390  
 DB 1230 GATGGGATAA 1239

## RESULT 5

AAAF85449

ID AAF85449 standard; cDNA; 1239 BP.

XX

AC AAF85449;

XX

23-JUL-2001 (first entry)

XX

DE Nucleotide sequence of a human motilin receptor polypeptide.

XX

KW Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW gastroparesis; irritable bowel syndrome; diarrhoea; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

CDS 1..1239

FT /\*tag= a

FT /note= "motilin receptor"

XX

PN WO200132710-A1.

XX

PD 10-MAY-2001.

XX

PF 25-OCT-2000; 2000WO-US029426.

XX

PR 29-OCT-1999; 99US-0162264P.

XX

PA (MERI ) MERCK &amp; CO INC.

XX

PI Tan C, McKee K;

XX

WPI; 2001-343479/36.

XX

DR P-PSDB; AAB68478.

XX

XX Novel polypeptides related to dog and rabbit motilin receptor

PT polypeptide, comprising unique regions from dog and motilin receptor

PT amino acid sequence, useful for identifying compounds for treating

PT diarrhea in humans.

XX

PS Disclosure; Page 34; 42pp; English.

XX

CC The present sequence encodes a human motilin receptor polypeptide. The  
 CC specification describes a unique sequence present in exon 1 of the dog  
 CC motilin receptor, which is not present in human or Sphaeroides nephelus  
 CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is  
 CC useful for measuring the ability of a compound to affect motilin receptor  
 CC activity. Motilin receptor polynucleotides and polypeptides are used to  
 CC identify therapeutic compounds which are useful for treating  
 CC gastrointestinal diseases and disorders such as gastric motility  
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea

XX

SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

XX

Query Match 77.6%; Score 1078; DB 4; Length 1239;

Best Local Similarity 89.1%; Pred. No. 7e-185;

DB

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;  
 QY 1 ATGGGAGCCCTTGGAAACGCGACGCGCCCGAGGGGCGCGGAGCGCGCTGGCCCC 60  
 DB 1 ATGGGAGCCCTTGGAAACGCGACGCGCCCGAGGGGCGCGGAGCGCGCTGGCCCC 60  
 QY 61 GCGTGCCTGCGCTTGGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGGTCCG 120  
 DB 61 GCGTGCCTGCGCTTGGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGGTCCG 120  
 QY 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 DB 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 QY 181 ATGCTGATCGGGCGCTACCGGACATCGGACACCACTTGTACCTTGGGCGAGCATG 240  
 DB 181 ATGCTGATCGGGCGCTACCGGACATCGGACACCACTTGTACCTTGGGCGAGCATG 240  
 QY 241 GCCGTGTCGACCTTACTCATCTGCTCGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 DB 241 GCCGTGTCGACCTTACTCATCTGCTCGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 QY 301 TCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 DB 301 TCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 QY 361 TGACCTTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 DB 361 TGACCTTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 QY 421 TGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 DB 421 TGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 QY 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 DB 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 QY 541 CAGGACCCCGCATCTCCGTAGTCCCGGCGCTCAATGGCACCCGCGCGAATGCCCTCTCTCG 600  
 DB 541 CAGGACCCCGCATCTCCGTAGTCCCGGCGCTCAATGGCACCCGCGCGAATGCCCTCTCTCG 600  
 QY 601 CCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 DB 601 CCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 QY 661 GGGCCCGAGAGCCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 DB 661 GGGCCCGAGAGCCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 QY 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 DB 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 QY 781 CTGTGCTCAGCATCTCTAGCGGCTCATCGGGGAGCTGTGGAGCAGCGCGCGCGCG 840  
 DB 781 CTGTGCTCAGCATCTCTAGCGGCTCATCGGGGAGCTGTGGAGCAGCGCGCGCGCGCGCG 840  
 QY 841 CTGCGAGCGCGCGCGCTCGGGGCGGAGAGGCGCACCGGCGAGCGCTCGCGCTCTCTG 900  
 DB 841 CTGCGAGCGCGCGCGCTCGGGGCGGAGAGGCGCACCGGCGAGCGCTCGCGCTCTCTG 900  
 QY 901 CGTAAGTGGAGCGCGCGTGGTTCACAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 DB 901 C----- 901  
 QY 961 GCGCAACCGCTGGGTCCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCC 1020  
 DB 902 ----- 901  
 QY 1021 TTCTCTATTTCGATTCAGCTCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 DB 902 -----TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 929

QY 1081 CTGTTGCCCTTCCAGTTCAGATCAATTTACATAAACACGGAAGATTCGCGGATGAT 1140  
 Db 930 CTGTTGCCCTTCCAGTTCGAGAAATCATTTACATAAACACGGAAGATTCGCGGATGAT 989  
 QY 1141 GTACTTCTCAGTACTTTAAATCGTTCGCTGCAACTTTTCTATCTGAGCGCATCTAT 1200  
 Db 990 GTACTTCTCAGTACTTTAAATCGTTCGCTGCAACTTTTCTATCTGAGCGCATCTAT 1049  
 QY 1201 CAACCAATCTCTACAACTCATTTCAAAGAAGTACAGAGCGGGCGCTTTAAACTGCT 1260  
 Db 1050 CAACCAATCTCTACAACTCATTTCAAAGAAGTACAGAGCGGGCGCTTTAAACTGCT 1109  
 QY 1261 GCTCGCAAGAGTCCAGCGCAGAGGCTTCCACAGAAGCAGGACACTCGCGGGGAAGT 1320  
 Db 1110 GCTCGCAAGAGTCCAGCGCAGAGGCTTCCACAGAAGCAGGACACTCGCGGGGAAGT 1169  
 QY 1321 TGCAGGGGACACTGGAGAGACACGGTGGGCTACACCGAGCAAGCGTCACTGAAGAC 1380  
 Db 1170 TGCAGGGGACACTGGAGAGACACGGTGGGCTACACCGAGCAAGCGTCACTGAAGAC 1229  
 QY 1381 CATGGGATAA 1390  
 Db 1230 CATGGGATAA 1239

## RESULT 6

AAF83683  
 ID AAF83683 standard; DNA; 1239 BP.

AC AAF83683;

XX 23-JUL-2001 (first entry)

DE Long form of motilin receptor, GPR-38A isoform encoding DNA.

XX zsig33; signal transduction; hormone; enzyme; neural development;  
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;  
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R; ds;  
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 1..1239  
 FT /\*tag=  
 FT /product= "GPR-38A"

PT WO200138355-A2.

PN 31-MAY-2001.

PD 22-NOV-2000; 2000WO-US032074.

PF 22-NOV-1999; 99US-0166765P.

PR (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI; 2001-355879/37.

DR P-PSDB; AAB62652.

XX Forming reversible peptide receptor complex for purifying cell and  
 PT peptides, stimulating signal transduction and modulating hormone  
 PT secretion, involves contacting a receptor with zsig33 polypeptide.

XX Disclosure; Page 102-104; 111pp; English.

XX The invention relates to a method of forming a reversible peptide-  
 CC receptor complex that involves providing an immobilized receptor, and  
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37

CC of AAB62649), where the receptor binds to the zsig33 peptide. The method  
 CC is useful for purifying cells, purifying a peptide, stimulating signal  
 CC transduction in a cell expressing a receptor. It is also useful for  
 CC modulating secretion of hormones, neural development and/or utilization,  
 CC gastric contractility, nutrient uptake, secretion of digestive and  
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor  
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth  
 CC hormone secretion in a mammal having a disease associated with abnormal  
 CC levels of growth hormone, such as osteoporosis, bone repair, bone  
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,  
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,  
 CC protein catabolic responses after surgery, cachexia, protein loss,  
 CC dwarfism, wound healing and ovulation induction, treating a mammal having  
 CC a metabolic disorder requiring neurological feedback, such as satiety  
 CC regulation, glucose absorption and metabolism and neuropathy-associated  
 CC gastrointestinal disorders, and stimulating glucose-induced insulin  
 CC release in a mammal. The present sequence represents the DNA encoding the  
 CC long form of motilin receptor, GPR-38A (one of the two isoforms of GPR38  
 CC which result from alternative splicing). GPR38 has homology to the human  
 CC G-protein coupled receptor, GHS-R

XX SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 77.6%; Score 1078; DB 4; Length 1239;

Best Local Similarity 89.1%; Pred. No. 7e-185;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

QY 1 ATGGGACGCCCCGGAACGGCAGCGAGCGCCCCGAGGGGGCGGAGCCCGCTGGGCC 60  
 Db 1 ATGGGACGCCCCGGAACGGCAGCGAGCGCCCCGAGGGGGCGGAGCCCGCTGGGCC 60  
 QY 61 GCGCTGCGCGCTTGGGACGAGCGCGCTGCTCGGCCCTTTCCCTGGGGCGCTGGTGGCG 120  
 Db 61 GCGCTGCGCGCTTGGGACGAGCGCGCTGCTCGGCCCTTTCCCTGGGGCGCTGGTGGCG 120  
 QY 121 GTGACCGCTGTGTGCTGTGCTGTTGCTGTGCGGGGTGAGCGGCAACGTTGACCGTG 180  
 Db 121 GTGACCGCTGTGTGCTGTGCTGTTGCTGTGCGGGGTGAGCGGCAACGTTGACCGTG 180  
 QY 181 ATGCTGATCGGGCGCTACCGGACATCGGACACCACTTGTACTCGGCGAGCATG 240  
 Db 181 ATGCTGATCGGGCGCTACCGGACATCGGACACCACTTGTACTCGGCGAGCATG 240  
 QY 241 GCCGTGTCCGACCTACTATCTCTGCTCGGGGTGCGCTGTGACCTGTACCGCTCTGGCGC 300  
 Db 241 GCCGTGTCCGACCTACTATCTCTGCTCGGGGTGCGCTGTGACCTGTACCGCTCTGGCGC 300  
 QY 301 TCGGGCGCTGGGTGTTGCGGCGCGCTGCTGTGCGCGCTGTCCTCTAGTGGGCGAGGCG 360  
 Db 301 TCGGGCGCTGGGTGTTGCGGCGCGCTGCTGTGCGCGCTGTCCTCTAGTGGGCGAGGCG 360  
 QY 361 TGCACCTACGCGCAGCTGTGCACATGACCGCGCTCAGCGCTCAGCGCTACCTGSCCATC 420  
 Db 361 TGCACCTACGCGCAGCTGTGCACATGACCGCGCTCAGCGCTCAGCGCTACCTGSCCATC 420  
 QY 421 TGCGCGCGCTTCCGCGCGCGCTTGTGTCAACCGCGCGCGCTCCGCGCGCTCATCGCT 480  
 Db 421 TGCGCGCGCTTCCGCGCGCGCTTGTGTCAACCGCGCGCGCTCCGCGCGCTCATCGCT 480  
 QY 481 GTGCTCTGGGCGGTGGCGCTGCTCTGTGCGCGCTGTCCTTCTTGTCTGTGGGCGTCCAG 540  
 Db 481 GTGCTCTGGGCGGTGGCGCTGCTCTGTGCGCGCTGTCCTTCTTGTCTGTGGGCGTCCAG 540  
 QY 541 CAGGACCCCGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGCATCGCTCCCTCG 600  
 Db 541 CAGGACCCCGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGCATCGCTCCCTCG 600  
 QY 601 CCTCTCGCTCTGTGCGCGCGCTCTCTGTGCTCTCGCGGGCGCCACCGCGCTCCCGCGCTCG 660  
 Db 601 CCTCTCGCTCTGTGCGCGCGCTCTCTGTGCTCTCGCGGGCGCCACCGCGCTCCCGCGCTCG 660  
 QY 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTACGCGCGCAATGCGGCGCCGAGCCCGCG 720



```
QY 421 TCCGCGCCGCTCCGCGCCGCGCTTGTGTACCGCGCGCGCGCTCCGCGCGCTCATCGCT 480
Db 421 TCCGCGCCGCTCCGCGCCGCGCTTGTGTACCGCGCGCGCGCTCCGCGCGCTCATCGCT 480
QY 481 GTGCTCTGGCGCGTGGCGCTGCTCTCTCCGCGTCCCTTCTTGTCTCTGCTGGCGTGGAG 540
Db 481 GTGCTCTGGCGCGTGGCGCTGCTCTCTCCGCGTCCCTTCTTGTCTCTGCTGGCGTGGAG 540
QY 541 CAGGACCCCGCATCTCCGTAAGTCCCGGCGCTCAATGACACCGCGCGGATCGCTCTCTCG 600
Db 541 CAGGACCCCGCATCTCCGTAAGTCCCGGCGCTCAATGACACCGCGCGGATCGCTCTCTCG 600
QY 601 CCTCTGCGCTGTCGCGCGCTCTCTGCGTCTGCGGGGCGCACCGCGTCCCGCGCGTGG 660
Db 601 CCTCTGCGCTGTCGCGCGCTCTCTGCGTCTGCGGGGCGCACCGCGTCCCGCGCGTGG 660
QY 661 GGGCCGAGACCGGGAGCGCGCGCTGTTTACGCGCGAATGCGCGCGCGAGCCCGCG 720
Db 661 GGGCCGAGACCGGGAGCGCGCGCTGTTTACGCGCGAATGCGCGCGCGAGCCCGCG 720
QY 721 CAGCTGGCGCGCTGCGTGTCTATGCTGTGGGTCAACCGCGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGCGCGCTGCGTGTCTATGCTGTGGGTCAACCGCGCTACTTCTTCTGCGCTTT 780
QY 781 CTGTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGGAGCAGCGCGCGCG 840
Db 781 CTGTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGGAGCAGCGCGCGCG 840
QY 841 CTGGAGCGCGCGCGCTCCGGCGGAGAGAGCGCACCGCGAGCGTCCGCGTCTG 900
Db 841 CTGGAGCGCGCGCGCTCCGGCGGAGAGAGCGCACCGCGAGCGTCCGCGTCTG 900
QY 901 CGTAAGTGGAGCGCGCGTGTTCACAGAGACCGCTGCTGCAAGTCCGCGCGCGGAC 960
Db 901 C----- 901
QY 961 GCGCAACGCTGGGTCCCTTCCCTGCTGCCAGCTCTGGCGCGCGCTTCCAGTCCC 1020
Db 902 ----- 901
QY 1021 TTTCTATTTTCAGATTCAGCCCTCCACCGCGTGGTGGTCTGGCATTTATAATTG 1080
Db 902 -----TGGTGGTGGTCTGGCATTTATAATTG 929
QY 1081 CTGGTGGCTTCCAGTGTGAGAAATCATTTACATAACACGGAAGATTCGCGGATGAT 1140
Db 930 CTGGTGGCTTCCAGTGTGAGAAATCATTTACATAACACGGAAGATTCGCGGATGAT 989
QY 1141 GTACTTCTCAGTACTTTAAATGATGCTGCTGCAACTTTTCTATCTGAGCGCATCTAT 1200
Db 990 GTACTTCTCAGTACTTTAAATGATGCTGCTGCAACTTTTCTATCTGAGCGCATCTAT 1049
QY 1201 CAACCAATCTCTACACCTTCAAGAGTACAGAGCGGCGGCTTTAACTGCT 1260
Db 1050 CAACCAATCTCTACACCTTCAAGAGTACAGAGCGGCGGCTTTAACTGCT 1109
QY 1261 GCTCGAAGGAGTCCAGCGCGAGGCTTCCAGAGAGGAGGACACTGCGGGGAGT 1320
Db 1110 GCTCGAAGGAGTCCAGCGCGAGGCTTCCAGAGAGGAGGACACTGCGGGGAGT 1169
QY 1321 TGCAGGGGACACTGGAGGAGACACGGTGGGTACACCGAGACAAGCGCTAAGTGAAGAC 1380
Db 1170 TGCAGGGGACACTGGAGGAGACACGGTGGGTACACCGAGACAAGCGCTAAGTGAAGAC 1229
QY 1381 GATGGGATAA 1390
Db 1230 GATGGGATAA 1239
```

## RESULT 8

ABZ42842

ID ABZ42842 standard; DNA; 1239 BP.

XX

AC ABZ42842;  
XX 04-MAR-2003 (first entry)  
XX Human motilin receptor GPR38 nucleotide SEQ ID NO:472.  
XX  
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
XX G protein-coupled receptor modulator; antibody; immune-related disease;  
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;  
XX immunological-related cell proliferative disease; autoimmune disease;  
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
XX ulcer; gene; ds.  
XX Homo sapiens.  
OS  
XX WO200261087-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 19-DEC-2001; 2001WO-US050107.  
XX  
XX 19-DEC-2000; 2000US-0257144P.  
XX  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
XX Burmer GC, Roush CL, Brown JP;  
XX WPI; 2003-046718/04.  
XX P-PSDB; ABP81993.  
XX  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
XX (GPCR), useful for diagnosing and designing drugs for treating conditions  
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
XX autoimmune diseases.  
XX  
XX Disclosure; Fig 1; 523pp; English.  
XX  
XX The present invention describes antigenic peptides (I) comprising: (a)  
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
XX acids. Also described: (1) an assay for the detection of a particular G  
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
XX and (2) an isolated antibody having high specificity and high affinity or  
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
XX antibody against a particular GPCR, and in the production of specific  
XX antibodies. The peptides and antibodies are also useful for detecting the  
XX presence or absence of corresponding GPCRs. The antigenic peptides for  
XX GPCRs and antibodies are useful for diagnosing and designing drugs for  
XX treating immune-related diseases, growth-related diseases, cell  
XX regeneration-related disease, immunological-related cell proliferative  
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,  
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host  
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory  
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
XX any other disorder in which GPCRs are involved. The antibodies may be  
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the  
XX exemplification of the present invention  
XX  
XX Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 77.6%; Score 1078; DB 8; Length 1239;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;



QY 1 ATGGGAGCCCTTGAAACGAGCAGCGCCCGAGGGGGCGCGGAGCCCGCCGTGGCCC 60  
Db 1 ATGGGAGCCCTTGAAACGAGCAGCGCCCGAGGGGGCGCGGAGCCCGCCGTGGCCC 60  
QY 61 GCGTGGCCGCTTGCGAGCGCGCGTGTCTGCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120  
Db 61 GCGTGGCCGCTTGCGAGCGCGCGTGTCTGCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120  
QY 121 GTGACCGCTGTGTGCTGTGTCTGTCTGCGGGGTGAGCGGCAACGTTGTGACCGGTG 180  
Db 121 GTGACCGCTGTGTGCTGTGTCTGTCTGCGGGGTGAGCGGCAACGTTGTGACCGGTG 180  
QY 181 ATGTGTATCGGGCGCTACCGGAGCATCGGACACCACTTGTACTTGGGAGCATG 240  
Db 181 ATGTGTATCGGGCGCTACCGGAGCATCGGAGACCACTTGTACTTGGGAGCATG 240  
QY 241 GCGTGTCCGACCTACTCATCTGTCTGCGGGGTGCGGTTCGACCTGTACCGCTCTGGCGC 300  
Db 241 GCGTGTCCGACCTACTCATCTGTCTGCGGGGTGCGGTTCGACCTGTACCGCTCTGGCGC 300  
QY 301 TCGGGCCCTGGGTGTTCGGGCGCTGTCTGCGCCCTGTCCCTTACGTGGGCGAGGGC 360  
Db 301 TCGGGCCCTGGGTGTTCGGGCGCTGTCTGCGCCCTGTCCCTTACGTGGGCGAGGGC 360  
QY 361 TGCACCTAGCGACGCTGTGCATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420  
Db 361 TGCACCTAGCGACGCTGTGCATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420  
QY 421 TCGCGCCGCTCGCGCCCGCTGTGTGTCAACCGGCGCGCTGCGCGCGCTCATCGCT 480  
Db 421 TCGCGCCGCTCGCGCCCGCTGTGTGTCAACCGGCGCGCTGCGCGCGCTCATCGCT 480  
QY 481 GTGCTGTGGGCGTGGCGCTGTCTGCGCGCTGCTTCTGTCTGTGGTGGGCTCGAG 540  
Db 481 GTGCTGTGGGCGTGGCGCTGTCTGCGCGCTGCTTCTGTCTGTGGTGGGCTCGAG 540  
QY 541 CAGGACCCCGGATCTCGGTAGTCCGGGCTCAATGACACCGCGCGATCGCTTCTCG 600  
Db 541 CAGGACCCCGGATCTCGGTAGTCCGGGCTCAATGACACCGCGCGATCGCTTCTCG 600  
QY 601 CCTCTGCGCTCGTCCGCGCTCTCTGTGTCTGCGGGCGCCACCGCGTCCCGCGCTCG 660  
Db 601 CCTCTGCGCTCGTCCGCGCTCTCTGTGTCTGCGGGCGCCACCGCGTCCCGCGCTCG 660  
QY 661 GGGCCCGAGACCGCGGAGCGCGCTGTTCAGCGCGAATGCGCGCGAGCCCGCG 720  
Db 661 GGGCCCGAGACCGCGGAGCGCGCTGTTCAGCGCGAATGCGCGCGAGCCCGCG 720  
QY 721 CAGCTGGGCGCTGCGTGTATGCTGTGGGTACACCGCTACTTCTTCTGCGCTTT 780  
Db 721 CAGCTGGGCGCTGCGTGTATGCTGTGGGTACACCGCTACTTCTTCTGCGCTTT 780  
QY 781 CTGTGCTCAGCATCTCTACGGGTCTATCGGGCGGAGCTGTGAGCAGCGCGCGCG 840  
Db 781 CTGTGCTCAGCATCTCTACGGGTCTATCGGGCGGAGCTGTGAGCAGCGCGCGCG 840  
QY 841 CTGCGAGCGCGCGCTCGGGCGGAGAGAGCGCCCGCGACCGTTCGGTCTG 900  
Db 841 CTGCGAGCGCGCGCTCGGGCGGAGAGAGCGCCCGCGACCGTTCGGTCTG 900  
QY 901 CGTAAGTGGAGCGCGCTGGTTCACAGCGCTGCTGCAAGCGCGCGCGCGGAGC 960  
Db 901 C----- 901  
QY 961 GCGCAACGCTGGGTGCCCTTCCCTGTCTGCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 1020  
Db 902 ----- 901  
QY 1021 TTCTCTATTTCGATTCCAGCTCCACCGCGTGTGTGTCTTGGCATTTATATTG 1080  
Db 902 -----TGTTGGTGGTTCGTCATTTATATTG 929

QY 1081 CTGTTGCCCTTCCACGTTGGCAGATCATTTACATAAACACGGAAGATTCCGGATGAT 1140  
Db 930 CTGTTGCCCTTCCACGTTGGCAGATCATTTACATAAACACGGAAGATTCCGGATGAT 989  
QY 1141 GTACTTCTCAGTACTTTAAACATCGTCTGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1200  
Db 990 GTACTTCTCAGTACTTTAAACATCGTCTGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1049  
QY 1201 CAACCCAACTCTTACAACTCATTTCAAAAGAGTACAGAGCGCGGCTTTAACTGCT 1260  
Db 1050 CAACCCAACTCTTACAACTCATTTCAAAAGAGTACAGAGCGCGGCTTTAACTGCT 1109  
QY 1261 GCTCGAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGT 1320  
Db 1110 GCTCGAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGT 1169  
QY 1321 TGCAGGGGACACTGAGGAGACACGTTGGGTACACCGAGACAAGCGTAACTGAAGAC 1380  
Db 1170 TGCAGGGGACACTGAGGAGACACGTTGGGTACACCGAGACAAGCGTAACTGAAGAC 1229  
QY 1381 GATGGGATAA 1390  
Db 1230 GATGGGATAA 1239  
RESULT 9  
ADN11760  
ID ADN11760 standard; cDNA; 1239 BP.  
XX  
AC ADN11760;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human motilin receptor GPR-38A coding sequence.  
XX  
KW ss; gene; human; zsig33; body weight; body mass; antibody; antagonist;  
KW gastrointestinal; antiinflammatory; antiulcer; vulnerary;  
KW growth hormone secretagogue; GHS-R; peptide-antibody complex;  
KW motilin receptor.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS Location/Qualifiers  
FT 1..1239  
FT /\*tag= a  
FT /product= "motilin receptor GPR38A"  
XX  
FN WO2004033645-A2.  
XX  
PD 22-APR-2004.  
XX  
PF 06-OCT-2003; 2003WO-US031804.  
XX  
PR 07-OCT-2002; 2002US-0416918P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;  
XX  
XX WPI; 2004-340913/31.  
DR P-PSDB; ADN11761.  
XX  
XX Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,  
XX inhibiting signal transduction in a cell expressing a growth hormone  
XX secretagogue receptor, or treating a metabolic disorder.  
XX  
PS Disclosure; Page 94-95; 100pp; English.  
XX  
CC The present invention relates to the use of a zsig33 peptide for forming  
CC a peptide-antibody complex, purifying a peptide, inhibiting signal  
CC transduction in a cell expressing a growth hormone secretagogue receptor  
CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite  
CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a



mammal, or treating a metabolic disorder. The peptide is useful for forming a peptide-antibody complex, purifying a peptide, inhibiting signal transduction in a cell expressing a GHS-R, decreasing fat deposition in a mammal, suppressing the appetite of a mammal, inhibiting growth hormone secretion in pituitary cells of a mammal, or treating a metabolic disorder. The zsig33 polypeptides can be used to study proliferation or differentiation in stomach, lung, pituitary, hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine, skeletal muscle or pancreas. They are also useful in delivering therapeutic agents. Zsig33 polypeptides, agonists and antagonists are also useful for promoting wound healing. The polypeptides, nucleic acids and antibodies are useful for diagnosing, treating or preventing disorders associated with gastric reflux, gastroparesis, modulation of secretion of pituitary hormones, including growth hormone, Cohn's disease, metabolic wasting, gastric ulcers, weight management, or degenerative disease. The present sequence is the human motilin receptor GPR38A coding sequence shown in the exemplification of the invention.

XX Query Match 77.6%; Score 1078; DB 12; Length 1239;  
Best Local Similarity 89.1%; Pred. No. 7e-185;  
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

QY 1 ATGGGACCCCTGGAGCGGAGCGAGCGCGCCCGAGGGGGCGGGAGCCCGCTGGGCC 60  
DB 1 ATGGGACCCCTGGAGCGGAGCGAGCGCGCCCGAGGGGGCGGGAGCCCGCTGGGCC 60  
QY 61 GCGTGGCCGCTTGGAGAGCGCGCTGCTGCCCTTTCCCTGGGGGGCGCTGGTGGC 120  
DB 61 GCGTGGCCGCTTGGAGAGCGCGCTGCTGCCCTTTCCCTGGGGGGCGCTGGTGGC 120  
QY 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
DB 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
QY 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACACCACTTGTACTCGGGAGCATG 240  
DB 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACCACTTGTACTCGGGAGCATG 240  
QY 241 GCGGTGTCGACCTACTCATCTGCTGGGGTGGCGTTTCGACCTGTACCGCTCTGGCG 300  
DB 241 GCGGTGTCGACCTACTCATCTGCTGGGGTGGCGTTTCGACCTGTACCGCTCTGGCG 300  
QY 301 TCGGGCCCTGGGTGTTGGGCGCTGCTCTGCGCGCTGTCCCTCTACGTGGGGAGGGC 360  
DB 301 TCGGGCCCTGGGTGTTGGGCGCTGCTCTGCGCGCTGTCCCTCTACGTGGGGAGGGC 360  
QY 361 TGCACCTAGCGACGCTGTCGACATGACCGGCTCAGCGTCGAGCGCTACCTGGCCATC 420  
DB 361 TGCACCTAGCGACGCTGTCGACATGACCGGCTCAGCGTCGAGCGCTACCTGGCCATC 420  
QY 421 TGGCGCCGCTCCGCGCCGCTGCTGTGCTACCGGGCGCGTCCGGCGCTCATCGCT 480  
DB 421 TGGCGCCGCTCCGCGCCGCTGCTGTGCTACCGGGCGCGTCCGGCGCTCATCGCT 480  
QY 481 GTGCTCTGGGCGCTGCTGCTCTGCGCGTCCCTTTCTTGTCTGCTGGGGTTCGAG 540  
DB 481 GTGCTCTGGGCGCTGCTGCTCTGCGCGTCCCTTTCTTGTCTGCTGGGGTTCGAG 540  
QY 541 CAGGACCCCGGATCTCCGTAGTCCGGGCTCAATGACACCGCGGATCGCTCTCTCG 600  
DB 541 CAGGACCCCGGATCTCCGTAGTCCGGGCTCAATGACACCGCGGATCGCTCTCTCG 600  
QY 601 CCTCTGCTGCTGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
DB 601 CCTCTGCTGCTGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
QY 661 GGGCCCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB 661 GGGCCCGAGACCGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
QY 721 CAGTGGGCGCGCTGCGTGTATGCTGTGGGTTCACCAACCGGCTACTTCTTCTGCGCTTT 780

DB 721 CAGTGGGCGCGCTGCGTGTATGCTGTGGGTTCACCAACCGGCTACTTCTTCTGCGCTTT 780  
QY 781 CTGTGCTCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGTGAGCAGCGCGGCGCG 840  
DB 781 CTGTGCTCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGTGAGCAGCGCGGCGCG 840  
QY 841 CTGGAGGCGCGCGCGCTCTGGGGGGAGAGAGCCACCGGAGACCGTTCGCGCTCTG 900  
DB 841 CTGGAGGCGCGCGCGCTCTGGGGGGAGAGAGCCACCGGAGACCGTTCGCGCTCTG 900  
QY 901 CGTAAGTGGAGCGCGCGTGGTTCAAAGACGCTTCCCTGCTGCGCGCGCGCGCGGAGCC 960  
DB 901 C----- 901  
QY 961 GCGCAACCGTGGGTTCCTTCCCTTCTGCTGCCCGAGCTCTGGGGCGCGCTTCAGCTGCC 1020  
DB 902 ----- 901  
QY 1021 TTTCTTATTCGATTTCAGCCTCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
DB 902 -----TGGTGGTGGTTCCTGCGATTTATAATTG 929  
QY 1081 CTGCTTGGCTTCCAGCTTGGCAGATCATTTACATAAACACGAGATTCGCGGATCAT 1140  
DB 930 CTGCTTGGCTTCCAGCTTGGCAGATCATTTACATAAACACGAGATTCGCGGATCAT 989  
QY 1141 GTACTTCTCTCAGTACTTTAAACATCGCTCTGCACTTTTCTATCTGAGCGCATCTAT 1200  
DB 990 GTACTTCTCTCAGTACTTTAAACATCGCTCTGCACTTTTCTATCTGAGCGCATCTAT 1049  
QY 1201 CAACCCAAATCTCTACAACTCATTTTCAAGAAAGTACAGAGCGCGCGCTTTAAACTGCT 1260  
DB 1050 CAACCCAAATCTCTACAACTCATTTTCAAGAAAGTACAGAGCGCGCGCTTTAAACTGCT 1109  
QY 1261 GCTCGAGGAGTTCAGGCGGAGAGGCTTCCAGAGAGGAGGACACTGCGGGGAGT 1320  
DB 1110 GCTCGAGGAGTTCAGGCGGAGAGGCTTCCAGAGAGGAGGACACTGCGGGGAGT 1169  
QY 1321 TGCAGGAGGACACTCGAGGAGAGACGCTGGGCTTACACCGAGACGAGCGCTAACGTGAAGAC 1380  
DB 1170 TGCAGGAGGACACTCGAGGAGAGACGCTGGGCTTACACCGAGACGAGCGCTAACGTGAAGAC 1229  
QY 1381 GATCGGATAA 1390  
DB 1230 GATCGGATAA 1239

RESULT 10  
ADO30072  
ID ADO30072 standard; cDNA; 1239 BP.  
XX AC ADO30072;  
XX DT 29-JUL-2004 (first entry)  
XX DE Human GPCR GPR38 polynucleotide, SEQ ID NO:1174.  
XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;  
KW cytosolic; antinflammatory; vasotropic; antidiarrhoeic; antidiabetic;  
KW CNS; central nervous system; respiratory; antianaemic; antiseborrhoeic;  
KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
KW gene; ss.





QY 961 GCGCAACGCTGGTCCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTCCAGCTCCC 1020  
 Db 902 ----- 901  
 QY 1021 TTCTCTATTTCGATTCACGCTCCACCGCCGTGGTGGTCTTGGCAATTTATAATTTG 1080  
 Db 902 -----TGGTGGTGGTCTTGGCAATTTATAATTTG 929  
 QY 1081 CTGGTTGCCCTTCCAGCTTGGCAGAAATCATTTACATAAACAGGAAATTCGCGATGAT 1140  
 Db 930 CTGGTTGCCCTTCCAGCTTGGCAGAAATCATTTACATAAACAGGAAATTCGCGATGAT 989  
 QY 1141 GTACTTCTCAGTACTTTAAACATCGCTCGCTGCAACTTTTCTATCTGAGCGCATCTAT 1200  
 Db 990 GTACTTCTCAGTACTTTAAACATCGCTCGCTGCAACTTTTCTATCTGAGCGCATCTAT 1049  
 QY 1201 CAACCAATCTCTCAACCTCATTTCAAAGAAATGACAGAGCGCGGCTTTAAACTGCT 1260  
 Db 1050 CAACCAATCTCTCAACCTCATTTCAAAGAAATGACAGAGCGCGGCTTTAAACTGCT 1109  
 QY 1261 GCTCCAGGAAAGTCCAGCGCGAGAGGCTTCCACAGAAGCGAGACACTGGGGGAAGT 1320  
 Db 1110 GCTCCAGGAAAGTCCAGCGCGAGAGGCTTCCACAGAAGCGAGACACTGGGGGAAGT 1169  
 QY 1321 TGCAGGGGACACTGGAGGAGACACGGTGGCTTACACCGAGACAAGCGCTAACGTGAAGAC 1380  
 Db 1170 TGCAGGGGACACTGGAGGAGACACGGTGGCTTACACCGAGACAAGCGCTAACGTGAAGAC 1229  
 QY 1381 GATGGGATAA 1390  
 Db 1230 GATGGGATAA 1239

## RESULT 12

AAI66989  
 ID AAI66989 standard; DNA; 1506 BP.  
 AC AAI66989;  
 XX  
 DT 30-JAN-2002 (first entry)  
 DE Human GPR38 variant GPR38V polypeptide encoding DNA.  
 KW GPR38V; variant; antibacterial; cytostatic; analgesic; antiasthmatic;  
 KW anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic;  
 KW antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant;  
 KW antiulcer; antiemetic; cardiac; vaccine; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1506  
 FT /\*tag= a  
 FT /product= "GPR38V"  
 XX  
 PN WO200164836-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US006277.  
 XX  
 PR 01-MAR-2000; 2000US-00516315.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 FI Elshourbagy N, Shabon U;  
 XX  
 DR WPI; 2001-638956/73.  
 DR P-PSDB; AAG65822.  
 XX  
 PT New human GPR38V polypeptide and polynucleotide, useful for treating e.g.  
 bacterial, fungal, protozoal and viral infections, cancers or allergies,

PT as vaccines, and for identifying agonists and antagonists potentially  
 XX useful in therapy.

PS Claim 2; Page 26; 32pp; English.

XX This DNA encodes a human GPR38 variant (GPR38V) polypeptide. GPR38V can  
 CC be expressed by standard recombinant methodology. The polynucleotides and  
 CC polypeptides are used in the treatment of bacterial, fungal, protozoal  
 CC and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,  
 CC diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart  
 CC failure, hypertension, urinary retentions, osteoporosis, allergies,  
 CC ulcers, migraine, psychotic and neurological disorders, or dyskinesias.  
 CC They are also useful for identifying agonists and antagonists that are  
 CC potentially useful in therapy, as vaccines to induce immunological  
 CC response in a mammal. The polypeptides may also be used as immunogens to  
 CC produce antibodies immunospecific for the polypeptides, and to identify  
 CC membrane bound or soluble receptors

XX Sequence 1506 BP; 207 A; 534 C; 509 G; 256 T; 0 U; 0 Other;

Query Match 77.6%; Score 1078; DB 4; Length 1506;

Best Local Similarity 89.1%; Pred. No. 7.1e-185;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

QY 1 ATGGGCGAGCCCTCGAAACGGCAGCGAGCGGCCCGGAGGGGGCGGAGCGCCCGCTGGGCC 60  
 Db 268 ATGGGCGAGCCCTCGAAACGGCAGCGAGCGGCCCGGAGGGGGCGGAGCGCCCGCTGGGCC 327  
 QY 61 GCGCTGCGCGCTTTCGACGAGCGCGCTGCTGCGCCCTTTCCCTTGGGGGGCGCTGGTGGCG 120  
 Db 328 GCGCTGCGCGCTTTCGACGAGCGCGCTGCTGCGCCCTTTCCCTTGGGGGGCGCTGGTGGCG 387  
 QY 121 GTGACCGCTGTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 Db 388 GTGACCGCTGTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447  
 QY 181 ATGCTGATCGGGCGCTACCGGGACATCGGACACCAACCACTTGATCTACCTGGGCGAGCATG 240  
 Db 448 ATGCTGATCGGGCGCTACCGGGACATCGGACACCAACCACTTGATCTACCTGGGCGAGCATG 507  
 QY 241 GCGGTGTCGACCTACTCATCTCTGCTCGGGGTGCGGTTCGACCTGTACCGCTCTGGCGC 300  
 Db 508 GCGGTGTCGACCTACTCATCTCTGCTCGGGGTGCGGTTCGACCTGTACCGCTCTGGCGC 567  
 QY 301 TCGGGCGCTCGGGGTGCGGGCGCTCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 Db 568 TCGGGCGCTCGGGGTGCGGGCGCTCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 627  
 QY 361 TGCACTTACGCCACCGCTGTGACATGACCGCGCTCAGCGCTCAGCGCTACTCTGGCCATC 420  
 Db 628 TGCACTTACGCCACCGCTGTGACATGACCGCGCTCAGCGCTCAGCGCTACTCTGGCCATC 687  
 QY 421 TGCCCGCGCTTCGCGCGCGCGCTTGGTACCGCGCGCGCGCTTCGCGCGCTCATCGCT 480  
 Db 688 TGCCCGCGCTTCGCGCGCGCGCTTGGTACCGCGCGCGCGCTTCGCGCGCTCATCGCT 747  
 QY 481 GTGCTCTGGGCGGTGCGCGCTGCTCTGCTGCGGTCCCTTCTGTTCTGTTGGGGGTGAG 540  
 Db 748 GTGCTCTGGGCGGTGCGCGCTGCTCTGCTGCGGTCCCTTCTGTTCTGTTGGGGGTGAG 807  
 QY 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGCGATCGCTCTCTCG 600  
 Db 808 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCACCGCGCGCGATCGCTCTCTCG 867  
 QY 601 CCTCTCGCTGTGCGCGCGCTCTCTGCGCTTCGCGGGCGCACCGCGTCCCGCGCGTGC 660  
 Db 868 CCTCTCGCTGTGCGCGCGCTCTCTGCGCTTCGCGGGCGCACCGCGTCCCGCGCGTGC 927  
 QY 661 GGGCGCGAGACCGCGGAGGCGCGCGCTGTTACGCGCGCAATCCGCGCGAGCCCGCG 720  
 Db 928 GGGCGCGAGACCGCGGAGGCGCGCGCTGTTACGCGCGCAATCCGCGCGAGCCCGCG 987  
 QY 721 CAGCTGGGCGCGCTGCGCTGCTCATGCTGTGGGTACACCGCGCTACTTCTTCTGCTGCTTT 780





Db 38376 TGCACCTAGCCACACCTGTCGACATGACCGGCTCAGCGTCGAGCGTACCTGCGCATC 38435  
Qy 421 TGCCCGCCGCTCCGCGCCGCTCTTGCTACCCGCGCGCGTCCGCGCGCTCATCGCT 480  
Db 38436 TGCCCGCCGCTCCGCGCCGCTCTTGCTACCCGCGCGCGTCCGCGCGCTCATCGCT 38495  
Qy 481 GTGCTCTGGCGCGTGGCGTGTCTCTGCGCGCTCTTGCTTGTGTTCTGTTGGGCGTGG 540  
Db 38496 GTGCTCTGGCGCGTGGCGTGTCTCTGCGCGCTCTTGCTTGTGTTCTGTTGGGCGTGG 38555  
Qy 541 CAGGACCCGCGATCTCCGTAGTCCCGGCGCTCAATGACCGCGCGATGCTCTCTCG 600  
Db 38556 CAGGACCCGCGATCTCCGTAGTCCCGGCGCTCAATGACCGCGCGATGCTCTCTCG 38615  
Qy 601 CCTCTGCGCTCTGCGCGCTCTCTGCGTCTGCGCGCGCGACCGCGCTCCCGCGCTCG 660  
Db 38616 CCTCTGCGCTCTGCGCGCTCTCTGCGTCTGCGCGCGCGACCGCGCTCCCGCGCTCG 38675  
Qy 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTTACGCGCGAATGCGCGCGAGCGCGCGCG 720  
Db 38676 GGGCCGAGACCGCGGAGCGCGCGCTGTTTACGCGCGAATGCGCGCGAGCGCGCGCG 38735  
Qy 721 CAGCTGGCGCGCTGCGTGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 38736 CAGCTGGCGCGCTGCGTGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38795  
Qy 781 CTGTCGCTCAGCATCTCTTACGGGCTCATCGGGGCTCATCGGGGCTCATCGGGGCTCAT 840  
Db 38796 CTGTCGCTCAGCATCTCTTACGGGCTCATCGGGGCTCATCGGGGCTCATCGGGGCTCAT 38855  
Qy 841 CTGCGAGCGCGCGCTCGGGGCGGAGAGCGCGCGAGAGCGCGCGAGAGCGCGCGCTGCTG 900  
Db 38856 CTGCGAGCGCGCGCTCGGGGCGGAGAGCGCGCGAGAGCGCGCGAGAGCGCGCGCTGCTG 38915  
Qy 901 CGTAAGTGGAGCGCGCTGTTTCCAAAGCGCTGCTGAGTCCGCGCGCGCGCGCGCGCG 960  
Db 38916 CGTAAGTGGAGCGCGCTGTTTCCAAAGCGCTGCTGAGTCCGCGCGCGCGCGCGCGCG 38975  
Qy 961 GCGCAACGCTGGGTCCTTCCCTGCTGCGCGCGAGCTGCGCGCGCGCTGCGCGCGCGCT 1020  
Db 38976 GCGCAACGCTGGGTCCTTCCCTGCTGCGCGCGAGCTGCGCGCGCGCTGCGCGCGCGCT 39035  
Qy 1021 TTTCTATTTCGATTCAGCGCTTCCACCGCGCG 1052  
Db 39036 TTTCTATTTCGATTCAGCGCTTCCACCGCGCG 39067

RESULT 15  
ID AAA46116  
XX AAA46116 standard; cDNA; 2040 BP.  
AC AAA46116;  
XX  
DT 22-AUG-2000 (first entry)  
XX  
DE Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.  
XX  
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
KW ss.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200022131-A2.  
PN  
XX  
PD 20-APR-2000.  
XX  
PF 13-OCT-1999; 99WO-US024065.  
XX  
PR 13-OCT-1998; 98US-00170496.  
PR 12-NOV-1998; 98US-0108029P.

PR 20-NOV-1998; 98US-0109213P.  
PR 27-NOV-1998; 98US-0110060P.  
PR 16-FEB-1999; 99US-0120416P.  
PR 26-FEB-1999; 99US-0121852P.  
PR 12-MAR-1999; 99US-0123944P.  
PR 12-MAR-1999; 99US-0123945P.  
PR 12-MAR-1999; 99US-0123946P.  
PR 12-MAR-1999; 99US-0123948P.  
PR 12-MAR-1999; 99US-0123949P.  
PR 12-MAR-1999; 99US-0123951P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0137127P.  
PR 28-MAY-1999; 99US-0137131P.  
PR 28-MAY-1999; 99US-0137567P.  
PR 29-JUN-1999; 99US-0141448P.  
PR 27-AUG-1999; 99US-0151114P.  
PR 03-SEP-1999; 99US-0152524P.  
PR 29-SEP-1999; 99US-0156555P.  
PR 29-SEP-1999; 99US-0156633P.  
PR 29-SEP-1999; 99US-0156634P.  
PR 29-SEP-1999; 99US-0156653P.  
PR 01-OCT-1999; 99US-0157280P.  
PR 01-OCT-1999; 99US-0157281P.  
PR 01-OCT-1999; 99US-0157282P.  
PR 01-OCT-1999; 99US-0157293P.  
PR 01-OCT-1999; 99US-0157294P.  
PR 12-OCT-1999; 99US-00416760.  
PR 12-OCT-1999; 99US-00417044.  
XX  
PA (AREN-) ARENA PHARM INC.  
XX  
PI Behan DP, Lehmann-Brulinsma K, Chalmers DT, Chen R, Dang HT;  
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
XX  
DR WPI; 2000-317986/27.  
DR P-PSDB; AAB02854.  
XX  
PT Non-endogenous, human G protein-coupled receptors for screening receptor,  
XX inverse or partial agonists useful as therapeutic agents.  
PS Example 2; Page 166-168; 187pp; English.  
XX  
CC The present invention describes transmembrane receptors, preferably human  
CC G protein coupled receptors (GPCR), for which the endogenous ligand is  
CC unknown (orphan GPCR receptors). More specifically the present invention  
CC relates to non-endogenous, constitutively activated versions of a human  
CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
CC identification of candidate compounds as receptors agonists, inverse  
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 2040 BP; 350 A; 630 C; 597 G; 463 T; 0 U; 0 Other;  
Query Match 75.3%; Score 1047.2; DB 3; Length 2040;  
Best Local Similarity 99.7%; Pred. No. 2.5e-179;  
Matches 1049; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ATGGGAGCCCTCGAAACGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Db 1 ATGGGAGCCCTCGAAACGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Qy 61 GCGCTGCGCGCTTGGAGCGAGCGCGCTGCTGCGCGCTTCCCTTGGGCGCGCTGCTGCGG 120  
Db 61 GCGCTGCGCGCTTGGAGCGAGCGCGCTGCTGCGCGCTTCCCTTGGGCGCGCTGCTGCGG 120  
Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Qy 181 ATGCTGATCGGGCGCTACCGGGAGCATGCGGACCAACCACTTGTACCTGGGCGAGCATG 240

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Db 181 ATGCTGATCGGCGCTACCGGACATCGGACACCAACTTGTACTCGGCGAGCATG 240
Qy 241 GCCGTGTCGAGACTACTCTGCTCGGCTCGGCTGCGCTGACCTGTACCGCTCTGCGGC 300
Db 241 GCCGTGTCGAGACTACTCTGCTCGGCTCGGCTGCGCTGACCTGTACCGCTCTGCGGC 300
Qy 301 TCGGGCCCTGGGTGTTTCGGGCGGCTGCTGCGGCTGCTCCCTCTAGCTGGGCGAGGGC 360
Db 301 TCGGGCCCTGGGTGTTTCGGGCGGCTGCTGCGGCTGCTCCCTCTAGCTGGGCGAGGGC 360
Qy 361 TGCACTACGGCACCGCTGCTGCACATGACCGGCTCAGCGTCGAGCGCTACTTGCCATC 420
Db 361 TGCACTACGGCACCGCTGCTGCACATGACCGGCTCAGCGTCGAGCGCTACTTGCCATC 420
Qy 421 TCGCGCCCGCTCGCGGCGGCTCTTGTGTACCGGCGCGGCTCGCGGCTCATCGCT 480
Db 421 TCGCGCCCGCTCGCGGCGGCTCTTGTGTACCGGCGCGGCTCGCGGCTCATCGCT 480
Qy 481 GTGCTCTGGGCGGCTGGCGCTGCTCTCGCGCTCCCTTCTTGTTCCTGCTGGGCTCGAG 540
Db 481 GTGCTCTGGGCGGCTGGCGCTGCTCTCGCGCTCCCTTCTTGTTCCTGCTGGGCTCGAG 540
Qy 541 CAGGACCCCGGATCTCCGTAGTCCCGGCGCTCAATGACCGCGCGGATCGCTCTCTCG 600
Db 541 CAGGACCCCGGATCTCCGTAGTCCCGGCGCTCAATGACCGCGCGGATCGCTCTCTCG 600
Qy 601 CCTCTCGGCTGTCGCGGCTCTCTGCTCTCGGCGGCGGCTCGCGGCTCGCGGCTCG 660
Db 601 CCTCTCGGCTGTCGCGGCTCTCTGCTCTCGGCGGCGGCTCGCGGCTCGCGGCTCG 660
Qy 661 GGGCCCGGAGACCGCGGAGCGCGGCTGTTTACCGCGGATGCGCGCGGAGCGCGCGG 720
Db 661 GGGCCCGGAGACCGCGGAGCGCGGCTGTTTACCGCGGATGCGCGCGGAGCGCGCGG 720
Qy 721 CAGCTGGGCGGCTCGGTGTCATGCTGGGTACACCGGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGGCTCGGTGTCATGCTGGGTACACCGGCTACTTCTTCTGCGCTTT 780
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGCGGCGGAGCGCGGCGG 840
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGCGGCGGAGCGCGGCGG 840
Qy 841 CTGCGAGGCGCGGCTCGGGCGGAGAGAGGACCGCGGAGAGCGCTCGCGCTCGTG 900
Db 841 CTGCGAGGCGCGGCTCGGGCGGAGAGAGGACCGCGGAGAGCGCTCGCGCTCGTG 900
Qy 901 CGTAAGTGAGCGCGGCTGTTCCAAAGACGCTGCTGCTGAGTCCGCGCGCGGAGAC 960
Db 901 CGTAAGTGAGCGCGGCTGTTCCAAAGACGCTGCTGCTGAGTCCGCGCGCGGAGAC 960
Qy 961 GCGCAACGCTGGTCCCTTCCCTGCTCGCGGAGCTGCGGCGGCGGCTTCCAGTCCC 1020
Db 961 GCGCAACGCTGGTCCCTTCCCTGCTCGCGGAGCTGCGGCGGCGGCTTCCAGTCCC 1020
Qy 1021 TTTCTATTTCGATCCAGCTCCACCGCGG 1052
Db 1021 TTTCTATTTCGATCCAGCTCCACCGCGG 1052
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Search completed: April 10, 2005, 23:50:42  
Job time : 755.96 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:55 ; Search time 228.453 Seconds  
(without alignments)  
9955.765 Million cell updates/sec

Title: US-09-719-485-4  
Perfect score: 1390  
Sequence: 1 atgggcagccctggaacgg.....acgtgaagacatgggataa 1390

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
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4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	20.4	283	3	US-08-993-088A-4
2	283	20.4	283	3	US-08-993-424B-4
3	283	20.4	283	4	US-09-603-680-4
4	248.2	17.9	1050	4	US-09-762-661A-1
5	234.8	16.9	1063	3	US-09-077-675A-1
6	234.8	16.9	1063	4	US-09-077-674-1
7	231.6	16.7	1095	4	US-09-743-475-2
8	231.6	16.7	4009	4	US-09-743-475-1
9	230	16.5	1029	3	US-09-077-675A-4
10	230	16.5	1029	4	US-09-077-674-4
11	229	16.5	250	4	US-09-016-434-359
12	228.8	16.5	1122	3	US-09-077-675A-9
13	228.8	16.5	1122	4	US-09-077-674-9
14	228.4	16.4	1092	3	US-09-077-675A-15
15	228.4	16.4	1092	4	US-09-077-674-15
16	228.4	16.4	3129	3	US-09-077-675A-14
17	228.4	16.4	3129	4	US-09-077-674-14
18	227.8	16.4	1088	3	US-09-077-675A-6
19	227.8	16.4	1088	4	US-09-077-674-6
20	227.8	16.4	1101	4	US-09-016-434-1148
21	227.8	16.4	1101	4	US-09-170-496D-87
22	227.8	16.4	1101	4	US-09-170-496D-209
23	227.8	16.4	1101	4	US-09-364-425B-44
24	153	11.0	836	3	US-09-077-675A-11
25	153	11.0	836	4	US-09-077-674-11
26	134.8	9.7	729	4	US-09-684-725-1
27	134.8	9.7	1239	4	US-09-949-016-4230

28 134.8 9.7 1248 3 US-09-545-944-1 Sequence 1, Appli  
29 134.8 9.7 1360 4 US-09-341-016A-2 Sequence 2, Appli  
30 134.8 9.7 16914 4 US-09-949-016-15972 Sequence 15972, A  
31 127 9.1 1233 4 US-09-826-509-536 Sequence 536, App  
32 127 9.1 1575 3 US-08-858-876A-1 Sequence 1, Appli  
33 127 9.1 1575 3 US-09-472-880-1 Sequence 1, Appli  
34 125.4 9.0 1342 3 US-08-832-399-1 Sequence 1, Appli  
35 125.4 9.0 1342 3 US-09-372-498-1 Sequence 1, Appli  
36 123 8.8 1257 4 US-09-826-509-534 Sequence 534, App  
37 123 8.8 4080 4 US-09-016-434-1346 Sequence 1346, App  
38 122.2 8.8 1529 3 US-08-858-876A-3 Sequence 3, Appli  
39 122.2 8.8 1529 3 US-09-472-880-3 Sequence 3, Appli  
40 122 8.8 1095 4 US-09-826-509-576 Sequence 576, App  
41 122 8.8 1285 4 US-08-016-434-1366 Sequence 1366, App  
42 120 8.6 1535 3 US-09-668-680-12 Sequence 12, Appli  
43 119 8.6 1212 4 US-09-170-496D-113 Sequence 113, App  
44 119 8.6 1212 4 US-09-170-496D-223 Sequence 223, App  
45 119 8.6 1212 4 US-09-743-742B-3 Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-08-993-088A-4  
; Sequence 4, Application US/08993088A  
; Patent No. 6287855  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Carina  
; APPLICANT: Sullivan, Kathleen  
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P. O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/993,088A  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/033,851  
; FILING DATE: 27-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 19846  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1958  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 283 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1...283  
; OTHER INFORMATION: cdna probe  
US-08-993-088A-4

Query Match	20.4%;	Score 283;	DB 3;	Length 283;
Best Local Similarity	100.0%;	Pred. No. 2.2e-50;		
Matches 283;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	206	TGCGGACCAACCAACTTGTACCTGGCGAGCATGGCCGTGTCCGACCTACTCATCTCTGC	265	
Db	1	TGCGGACCAACCAACTTGTACCTGGCGAGCATGGCCGTGTCCGACCTACTCATCTCTGC	60	
QY	266	TCGGGTGCGCGTTCGACCTCTACCGCTCTCGGGCTCGCGGCCCTGGGTGTCGGGGCCG	325	
Db	61	TCGGGTGCGCGTTCGACCTCTACCGCTCTCGGGCTCGCGGCCCTGGGTGTCGGGGCCG	120	
QY	326	TGCTCTGCCGCCCTGTCCCTCTACGTGGCGAGGGCTGCACCTACGCACCGTGTGTGCACA	385	
Db	121	TGCTCTGCCGCCCTGTCCCTCTACGTGGCGAGGGCTGCACCTACGCACCGTGTGTGCACA	180	
QY	386	TGACCGCGCTCAGCGTTCAGCGGTACTCTGGCCATCTCGCGCCGCTCCGGCCCGCGCTCT	445	
Db	181	TGACCGCGCTCAGCGTTCAGCGGTACTCTGGCCATCTCGCGCCGCTCCGGCCCGCGCTCT	240	
QY	446	TGCTACCCGGCGCGCGTTCGGCGGCTCATTCGCTGTGCTGTG	488	
Db	241	TGCTACCCGGCGCGCGTTCGGCGGCTCATTCGCTGTGCTGTG	283	

## RESULT 2

US-08-993-424B-4  
Sequence 4, Application US/08993424B  
Patent No. 6337206  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Kolakowski, Lee F., Jr.  
TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALT2 AND  
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,424B  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,851  
FILING DATE: 27-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846NP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 283 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...283  
OTHER INFORMATION: cDNA probe

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US-08-993-424B-4
Query Match      20.4%; Score 283; DB 3; Length 20
Best Local Similarity 100.0%; Pred. No. 2.2e-50;
Matches 283; Conservative 0; Mismatches 0; Indels

Qy      206  TCGGGACACCCACCAACTTGTACTTGGCAGCATGGCCGTGTCCGAC
Db      1   TCGGGACACCCACCAACTTGTACTTGGCAGCATGGCCGTGTCCGAC

Qy      266  TCGGGCTGCGGTTTCGACTGTACCGCTCTGGCGCTCGCGGCCCTCGGG
Db      61  TCGGGCTGCGGTTTCGACTGTACCGCTCTGGCGCTCGCGGCCCTCGGG

Qy      326  TGCTCTCGCGCCTGTGCCTCTTACCTGGCGGAGGGCTGCACCTACGCC
Db      121  TGCTCTCGCGCCTGTGCCTCTTACCTGGCGGAGGGCTGCACCTACGCC

Qy      386  TGACCGGGCTCAGCGGTGAGCGCTACCTGGCCATCTGCGCGCCCGCTCC
Db      181  TGACCGGGCTCAGCGGTGAGCGCTACCTGGCCATCTGCGCGCCCGCTCC

Qy      446  TGGTACCCCGCGCCCGGTCCGCGGCTCATCGCTGTGCTCTG 488
Db      241  TGGTACCCCGCGCGCGGTCCGCGGCTCATCGCTGTGCTCTG 283

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### RESULT 3

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US-09-603-680-4
; Sequence 4, Application US/09603680
; Patent No. 6544753
;
GENERAL INFORMATION:
;
APPLICANT: Tan, Carina
;
; Sullivan, Kathleen
;
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; NUCLEOTIDES ENCODING SAME
;
NUMBER OF SEQUENCES: 20
;
CORRESPONDENCE ADDRESS:
;
ADDRESS: Merck & Co., Inc.
;
STREET: P.O. Box 2000, 126 E. Lincoln Ave
;
CITY: Rahway
;
STATE: NJ
;
COUNTRY: USA
;
ZIP: 07065-0900
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Diskette
;
COMPUTER: IBM Compatible
;
OPERATING SYSTEM: Windows
;
SOFTWARE: PatsEQ for Windows Version 2.0b
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/09/603,680
;
FILING DATE: 26-Jun-2000
;
CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: 60/033,851
;
FILING DATE: 27-DEC-1996
;
APPLICATION NUMBER: 08/993,088
;
FILING DATE: 18-DEC-1997
;
ATTORNEY/AGENT INFORMATION:
;
NAME: Heber, Sheldon O.
;
REGISTRATION NUMBER: 38,179
;
REFERENCE/DOCKET NUMBER: 19846 CA
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: 732-594-1958
;
TELEFAX: 732-594-4720
;
TELEX: <Unknown>
;
INFORMATION FOR SEQ ID NO: 4:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 283 base pairs
;
TYPE: nucleic acid
;
STRANDEDNESS: single
;
TOPOLOGY: linear
;
MOLECULE TYPE: Other

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FEATURE:  
NAME/KEY: Other  
LOCATION: 1...283  
OTHER INFORMATION: cDNA probe  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-603-680-4

Query Match 20.4%; Score 283; DB 4; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2.2e-50;  
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 TGCAGCACCACCAACCTTGACCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTCCTGCGGC 265  
Db 1 TGCAGCACCACCAACCTTGACCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTCCTGCGGC 60

Qy 266 TCGGGCTGCGGTTCGACCTGTACCGCTCTGCGGCTCGCGGCTCGGGTGTTCGGGCGGC 325  
Db 61 TCGGGCTGCGGTTCGACCTGTACCGCTCTGCGGCTCGGGTGTTCGGGCGGC 120

Qy 326 TGCTTGCGGCTGTCCCTCTACGTGGGCGAGGCTGCACTACGCCAGGCTGTGTCGACA 385  
Db 121 TGCTTGCGGCTGTCCCTCTACGTGGGCGAGGCTGCACTACGCCAGGCTGTGTCACA 180

Qy 386 TGACCGGCTCAGCGTCGAGCGCTACCTGGCCATCTGCGGCGCTCGCGCCGCTCT 445  
Db 181 TGACCGGCTCAGCGTCGAGCGCTACCTGGCCATCTGCGGCGCTCGCGCCGCTCT 445

Qy 446 TGGTCACCGCGCGCGCTCGCGGCTCATCGCTGTGCTGTG 488  
Db 241 TGGTCACCGCGCGCGCTCGCGGCTCATCGCTGTGCTGTG 283

## RESULT 4

US-09-762-661A-1  
; Sequence 1, Application US/09762661A  
; Patent No. 6645726  
; GENERAL INFORMATION:  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Palyha, Oksana C.  
; APPLICANT: Smith, Roy G.  
; APPLICANT: Tan, Carina P.  
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE  
; FILE REFERENCE: 20207P  
; CURRENT APPLICATION NUMBER: US/09/762,661A  
; CURRENT FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/17915  
; PRIOR FILING DATE: 1999-08-06  
; PRIOR APPLICATION NUMBER: 60/095,960  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1050  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(1050)  
; OTHER INFORMATION: n = A,T,C or G

US-09-762-661A-1

Query Match 17.9%; Score 248.2; DB 4; Length 1050;  
Best Local Similarity 65.9%; Pred. No. 5.8e-43;  
Matches 375; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

Qy 92 GCGCCCTTTCCCTGCGGGCGCTGTGGCGGTGACCGCTGTGTGCTGTGCTGTGCTGTGCTG 151  
Db 56 CGCTGTTCCTCCGCGCGCTGTGGCGGCGTGCACGCCACCTGTGCGGTGTTCGCG 115

Qy 152 TCGGGGTGAGCGCAACCTGTGTGACCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 211  
Db 116 TGGCGGTGCGCGGCAACCTGTGTGACCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 175

Qy 212 CCACACCAACTTGTACCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTCCTGCTGCGGC 271  
Db 176 CCACACCAACTTGTACCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTCCTGCTGCA 235

Qy 272 TCGGTTTCGACCTGTACCGCTCTGGCGCTCGCGGCTGGGTGTTTCGGGCGCTGCTCT 331  
Db 236 TCGGCTCGACCTGTGTGCGCTGTGGCAGTACCGGCTTGGACCTTCGGGCGACCTGCTCT 295

Qy 332 GCGGCTTGCCTCTTACGTGGGCGAGGCTGCACCTAGCCACGCTGTGTCACATGACCG 391  
Db 296 GCAAACTCTTCAGTTCGTGAGCGAGGCTGCACCTAGCCACGCTGTCCACATCACGG 355

Qy 392 CGCTCAGGCTCGAGGCTACTTGGCCATCTGCGGCTCGCGGCTCGCGGCTGTGCTGTC 451  
Db 356 CGCTCAGGCTCGAGGCTACTTTCGCCATCTGCTTCCCGCTCGCGGCTGCTGCTGCA 415

Qy 452 CCGGCGCGGCTCGCGGCTCATCGCTGTGCTGTGGGCGTGGCGCTGCTCTGCGG 511  
Db 416 CCAAGGCGCGCTGAAGCTGCGCTTGGGCGCTGCGGCTTCTGACGCGCG 475

Qy 512 GTCCCTTCTTCTTCTGCTGGGCGTGCAGCAGGACCCCGGCTC-TCGCTAGTCCCGGCG 570  
Db 476 GGGCCATCTTCTGCTGTGGGCGTGGAGCAGAGAACCGACCCCGGAGACCCC 535

Qy 571 CTCAATGCAACCGCGGATCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 630  
Db 536 CGAGTTCGCGGCGCACCGAGTTCGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTG 595

Qy 631 TCGGCGGCGCGCACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659  
Db 596 TGTCCAGCGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624

## RESULT 5

US-09-077-675A-1  
; Sequence 1, Application US/09077675A  
; Patent No. 6242199  
; GENERAL INFORMATION:  
; APPLICANT: Pai, Lee-Yuh  
; APPLICANT: Feighner, Scott C.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Pong, Sheng-Shung  
; APPLICANT: Van Der Ploeg, Leonardus H.T.  
; TITLE OF INVENTION: RECEPTOR ASSAY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,675A  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19590P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:



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; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-743-475-2

Query Match      16.7%; Score 231.6; DB 4; Length 1095;
Best Local Similarity 68.8%; Pred. No. 1.8e-39;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 92 CGCCCTTTCCCTGGGGCGCTGGTGC CGGTGACCGTGTGATCGGCGCTACCGGACATGCGGA 211
Db 104 CACTGTTCCCGCGCGCTGCTGGCGGCGTCACTGCCACCTGCTGCGGCTCTTCTGTTGG 163

Qy 152 TCGGGGTGAGCGGCAACGTGTGACCGTGTGATCGGCGCTACCGGACATGCGGA 211
Db 164 TGGGCATCTCGGGCAACCTGCTCACCATGCTGTGTGTTGTCCTTCCCGCTTCCGCGAGCTGCGCA 223

Qy 212 CCACCACCAACTTGTACCTGGGCGCATGGCGGTGTCGACCTACTCATCTGCTCGGGC 271
Db 224 CCACCACCAACTTGTACCTATCCAGATGGCGCTTCTCGATCTGCTCATCTTCTGTGCA 283

Qy 272 TGCCGTTCCGACCTGTACCGCTCTGCGGCTCGCGCCCTGGGTGTTGGGCGCGTGTCT 331
Db 284 TGCCGTTCCGACCTGTGCGCTCTGCGAGTATCGGCGCTTGGAACTTGGCGACCTGTCT 343

Qy 332 GCCGCTGTCTCTACGTGGCGAGGGGTGACCTAGCCACGCTGCTGCTGACATGACCG 391
Db 344 GCAAACTCTTCCAGTTTGTACGAGAGAGTGCACCTAGCCACGCTCTCACCATCACCG 403

Qy 392 GCCTCAGGTGAGCGCTACCTGCGCATCTGCGCGCCCTGCGGTGTTGGGCGCGTGTGTC 451
Db 404 CCGTGAAGCTGTGAAGCTGTGTCATCTTGTGTCATCTGGCGCGTGGCTTCTGCGCGCGG 523

Qy 452 CCGCGCGCGCTCGCGCGCTCATCGTGTGCTTGGGCGCGTGGCGCTGCTCTGCGCG 511
Db 464 CCAAGGCGCGTGAAGCTGTGTCATCTTGTGTCATCTGGCGCGTGGCTTCTGCGCGCGG 523

Qy 512 GTCCCTTTCTTCTTCTGTTGGCGCTGCGAGCAGGACCCCGCA 553
Db 524 GCGCCATCTTCTGTTGGTGGCGTGGAGCAGGACGAGACGCA 565
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## RESULT 8

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US-09-743-475-1
; Sequence 1, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4009
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-743-475-1
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Query Match      16.7%; Score 231.6; DB 4; Length 4009;
Best Local Similarity 68.8%; Pred. No. 2.3e-39;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 92 CGCCCTTTCCCTGGGGCGCTGGTGC CGGTGACCGTGTGATCGGCGCTACCGGACATGCGGA 211
Db 605 CACTGTTCCCGCGCGCTGCTGGCGGCGTCACTGCCACCTGCTGCGGCTCTTCTGTTGG 664

Qy 152 TCGGGGTGAGCGGCAACGTGTGACCGTGTGATCGGCGCTACCGGACATGCGGA 211
Db 665 TGGGCATCTCGGGCAACCTGCTCACCATGCTGTGTGTTGTCCTTCCCGCTTCCGCGAGCTGCGCA 724

Qy 212 CCACCACCAACTTGTACCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTGCTCGGGC 271
Db 725 CCACCACCAACTTGTACCTATCCAGATGGCGCTTCTCGATCTGCTCATCTTCTGTGCA 784

Qy 272 TGCCGTTCCGACCTGTACCGCTCTGCGGCTCGCGCCCTGGGTGTTGGGCGCGTGTCT 331
Db 785 TGCCGTTCCGACCTGTGCGCTCTGCGAGTATCGGCGCTTGGAACTTGGCGGACCTGTCT 844

Qy 332 GCCGCTGTCTCTACGTGGCGAGGGGTGACCTAGCCACGCTGCTGACATGACCG 391
Db 845 GCAAACTCTTCCAGTTTGTACGAGAGAGTGCACCTAGCCACGCTCTCACCATCACCG 904

Qy 392 CGCTCAGGTGAGCGCTACCTGCGCATCTGCGCGCCCTGCGCGCCCGCTGTTGGTCA 451
Db 905 CGCTGAGCGTGGAGCGCTACTTCCCATCTCTCTTCCCGCTGCGGCGCAAGGTGGTCA 964

Qy 452 CCGCGCGCGCTCGCGCGCTCATCGTGTGCTTGGGCGCGTGGCGCTGCTCTGCGCG 511
Db 965 CCAAGGCGCGTGAAGCTGTGTCATCTTGTGTCATCTGGGCGCTGGCTTCTGCGCGCGG 1024

Qy 512 GTCCCTTTCTTCTTCTGTTGGCGCTGCGAGCAGGACCCCGCA 553
Db 1025 GCGCCATCTTCTGTTGGTGGCGTGGAGCAGGACGAGACGCA 1066
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## RESULT 9

```
US-09-077-675A-4
; Sequence 4, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 359:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: THPINOT01  
CLONE: 2018536  
US-09-016-434-359

Query Match 16.5%; Score 229; DB 4; Length 250;  
Best Local Similarity 98.8%; Pred. No. 4.6e-39;  
Matches 240; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1148 TCTCAGTACTTTAAACATCGTCTCTGCAACTTTTCTATCTGAGCGCATCTATCAACCCA 1207  
Db 1 TCTCAGTACTTTAAACATCGTCTCTGCAACTTTTCTATCTGAGCGCATCTATCAACCCA 60  
QY 1208 ATCTCTTACAACCTCATTTTCAAGAAGTACAGAGCGCGGCTTTAAACTGCTGCTCGCA 1267  
Db 61 ATCTCTTACAACCTCATTTTCAAGAAGTACAGAGCGCGGCTTTAAACTGCTGCTCGCA 120  
QY 1268 AGGAGTCCAGGCCGAGAGGCTTCCACAGACGAGGACACTGCGGGGAGTTTCAGGG 1327  
Db 121 AGGAGTCCAGGCCGAGAGG-TTCACAGACGAGGACACTGCGGGGAGTTTCAGGG 179  
QY 1328 GACACTGGAGGAGACACGCTGGGCTACACCGAGACAAGCGCTTAAAGTGAAGACGATGGGA 1387  
Db 180 GACACTGGAGGAGACACGCTGGGCTACACCGAGACAAGCGCTTAAAGTGAAGACGATGGGA 239  
QY 1388 TAA 1390  
Db 240 TAA 242

RESULT 12  
US-09-077-675A-9  
; Sequence 9, Application US/09077675A

Patent No. 6242199  
GENERAL INFORMATION:  
APPLICANT: Pai, Lee-Yuh  
APPLICANT: Feighner, Scott C.  
APPLICANT: Howard, Andrew D.  
APPLICANT: Pong, Sheng-Shung  
APPLICANT: Van Der Ploeg, Leonardus H.T.  
TITLE OF INVENTION: RECEPTOR ASSAY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/077,675A  
FILING DATE: 3-JUN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cocuzzo, Anna L.  
REGISTRATION NUMBER: 42,452  
REFERENCE/DOCKET NUMBER: 19590P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1273  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1122 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-077-675A-9

Query Match 16.5%; Score 228.8; DB 3; Length 1122;  
Best Local Similarity 57.9%; Pred. No. 6.9e-39;  
Matches 424; Conservative 0; Mismatches 307; Indels 1; Gaps 1;  
QY 93 GCCCTTTCCCTGGGGGCGCTGGTGCCGGTGACCGCTGTGTGCCTGTGCTGTTCGTGT 152  
Db 360 GCTCTTCCCGCGCGCTGCTGGCGGCGTCACAGCCACCTGCGTGGCACCTCTTCGTGT 419  
QY 153 CGGGGTGAGCGGCAACGTGTGTGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 212  
Db 420 GGGTATCGCTGGCAACCTGCTCACCATGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 479  
QY 213 CACCACCAACTTGTACCTGGCGGCGAGCATGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 272  
Db 480 CACCACCAACTTGTACCTGT 539  
QY 273 GCCGTTCGACCTGTACCGCCTCTGGCGCTCGCGGCTGTGGGTGTGTGGGCGCGCTGTCTGT 332  
Db 540 GCCCTTGGACCTCGTTCCCTTGGCAGTACCGGCGCTGGAACTTCCGCGGACCTCTCTGT 599  
QY 333 CGGCTGTGCTCTTACGTGGGCGAGGCTGACCTTACGCCACGCTGTGTGTGTGTGTGTGTGTGT 392  
Db 600 CAAACTCTTCAATTCGTTCAGTGAGCTGACCTTACGCCACGCTGTGTGTGTGTGTGTGTGTGT 659  
QY 393 GCTCAGCGTGGCGCTACCTGGCGCATCTGGCGCGCTGTGGCGCTGTGGCGCGCTGTGTGTGT 452  
Db 660 GCTCAGCGTGGCGCTACCTGT 719

QY 453 CCGGCGCCGCGCTCCGCGCTCATCGCTGTGCTCTGGCGCGCTGCTCTCTGCGCG 512  
Db |||||  
720 CAAGGGCGGGTGAAGCTGGTCACTTCTGCTGCTGGCGCGCTCTCTGCGCGCGG 779  
QY 513 TCCTTCTTGTCTGCTGGTGGGCTGAGCAGAGACCCCGGCTCT-CCGTAGTCCGCGCG 571  
Db |||||  
780 GCCCATCTTCTGCTAGTGGGCTGGAGCAGAGAACCGCACCCCTTGGGACACCAA 839  
QY 572 TCAATGGACCGCGGATCGCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 631  
Db |||||  
840 CAGAGTCCGCGCCACCGAGTTGGGCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 899  
QY 632 CCGCGCGCGCACCGCGCTCCCGCGCTGGGCGCGGAGACCGCGCGCGCGCTGT 691  
Db |||||  
900 GTCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 959  
QY 692 TCAGCGCGGAATGCGCGCGCGAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 751  
Db |||||  
960 CAGGAAGCTGTGGCGAGGAGCGCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019  
QY 752 TCACACCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 811  
Db |||||  
1020 GAACACAAAGAAACCGTGAAATGCTGGTGGGCTCAGCGCGCTCAGCGCGCTTCTCT 1079  
QY 812 GCGGGAGCTGT 823  
Db |||||  
1080 CCGGGTCTAT 1091

## RESULT 13

US-09-077-674-9  
; Sequence 9, Application US/09077674  
; Patent No. 6531314  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,674  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19589P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1122 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-077-674-9  
Query Match 16.5%; Score 228.8; DB 4; Length 1122;  
Best Local Similarity 57.9%; Pred. No. 6.9e-39;  
Matches 424; Conservative 0; Mismatches 307; Indels 1; Gaps 1;  
QY 93 GCCCTTCCCTGGGCGCGCTGGTCCGCTGACCGCTGTGCTGCTGCTGCTGCTGCTGCT 152  
Db GCTCTTCCCGCGCGCTGCTGGCGCGCTCACAGCCACCTGCGTGGGCTCTTCTTCTGCT 419  
QY 153 CGGGGTGAGCGCAACGTTGACCTGGCGCTGATCGCTGATCGGGCGCTACCGGACATGCGGAC 212  
Db |||||  
420 GGGTATCGCTGGCAACCTGCTCACATGCTGGTGTGCGGCTTCCCGAGCTGCGGAC 479  
QY 213 CACCACCAACTTGTACCTGGCGCAGCATGGCGCTGTCCGACCTACTCATCTCTGCTGGGCT 272  
Db |||||  
480 CACCACCAACTTGTACCTGGCGCAGCATGGCGCTTCTCCGATCTGCTCATCTTCTCTGCT 539  
QY 273 GCGTTCGACCTGTACCGCTCTGCGCTCGCGGCTTGGTGTGCGGCGCTGCTGCTGCTG 332  
Db |||||  
540 GCGCTGACCTCGTTGCGCTCTGCGCTACCGGCTTGGAACTTCCGCGACCTCTCTCTG 599  
QY 333 CCGCTGCTCTACGTTGGCGGCTGACCTAGCCACCTAGCCACCTGCTGCAATGACCGC 392  
Db |||||  
600 CAACTTTCANATTCGTGAGCTGACCTAGCCACCTAGCCACCTGCTGCAATGACCGC 659  
QY 393 GCTCAGCTGAGCGCTACCTGGCGCATCTGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCT 452  
Db |||||  
660 GCTGAGCTGAGCGCTACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719  
QY 453 CCGCGCGCGCTCGCGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512  
Db |||||  
720 CAGCGCGCGTGAAGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779  
QY 513 TCCTTCTTGTCTGTTGGTGGCGCTCGAGCAGGACCCCGCGCATCT-CCGTAGTCCCGGGCC 571  
Db |||||  
780 GCCCATCTTCTGCTAGTTCGGGTGGAGCAGAGAACCGCACCCCTTGGGACACCAA 839  
QY 572 TCAATGGACCGCGGATCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 631  
Db |||||  
840 CAGTTCGCGCGCCACCGAGTTTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899  
QY 632 CCGCGCGCGCACCGCGCTCCCGCGCTGCGGCGCGGAGACCGCGGAGGCGCGGCGCTGT 691  
Db |||||  
900 GTCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 959  
QY 692 TCAGCGCGGAATGCGCGCGGAGCGCGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 751  
Db |||||  
960 CAGGAGCTGTGGGAGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019  
QY 752 TCACACCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 811  
Db |||||  
1020 GAACCAAGCAACCGTGAATGCTGGTGGGCTTCTCAGCGCGGCTCAGCGCTTCTCT 1079  
QY 812 GCGGGAGCTGT 823  
Db |||||  
1080 CCGGGTCTAT 1091

## RESULT 14

US-09-077-675A-15  
; Sequence 15, Application US/09077675A  
; Patent No. 6242199  
; GENERAL INFORMATION:  
; APPLICANT: Pai, Lee-Yuh  
; APPLICANT: Feighner, Scott C.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Pong, Sheng-Shung  
; APPLICANT: Van Der Ploeg, Leonardus H.T.



RESULT 15  
 US-09-077-674-15  
 ; Sequence 15, Application US/09077674  
 ; Patent No. 6531314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Atena, Joseph P.  
 ; APPLICANT: Cully, Doris F.  
 ; APPLICANT: Feighner, Scott D.  
 ; APPLICANT: Howard, Andrew D.  
 ; APPLICANT: Liberator, Paul A.  
 ; APPLICANT: Schaeffer, James M.  
 ; APPLICANT: Van Der Ploeg, Leonardus  
 TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY  
 ;  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065-0900  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/077,674  
 ; FILING DATE: 3-JUN-1998  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cocuzzo, Anna L.  
 ; REGISTRATION NUMBER: 42,452  
 ; REFERENCE/DOCKET NUMBER: 19589P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 732-594-1273  
 ; TELEFAX: 732-594-4720  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1092 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-09-077-674-15

[illegible]

Db	344	GCAAACTCTTCCAGATTTTGTACGAGAGCTCACTACGCCACGGTCTCTCAACATCACCG	403
Qy	392	CGCTCAGGTCGAGCGGTACTCGTGCCATCTCGCGCCGCTCCGGCGCCGCGTCTTGTC	451
Db	404	CGCTGAGCGTCGAGCGGTACTTCCGCCATCTGCTTCCCTCTCGGGGCCAAGGTGGTGTC	463
Qy	452	CCGGCGCCGCGTCCGGCGGTCACTCGGTGCTCTGSGCGTGGCGGTCTCTCTGCGG	511
Db	464	CTAAGGGCCGCGTGAAGCTGTGCATCTTGTGCATCTGGCGCGTGCTTCTTGACGCGGG	523
Qy	512	GTCCTTCTTGTTCCTGGTGGCGTCGAGCAGGACCCCGCA	553
Db	524	GGCCCATCTTCGTGCTGGTGGCGGTGAGACAGAAACGGCA	565

Search completed: April 11, 2005, 13:13:33  
Job time : 229.453 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1161	83.5	1161	18	US-10-679-813-11	Sequence 11, Appl
2	1078	77.6	1239	15	US-10-225-567A-472	Sequence 472, App
3	1078	77.6	1239	15	US-10-230-078-13	Sequence 13, Appl
4	1078	77.6	1239	15	US-10-230-078-14	Sequence 14, Appl
5	1078	77.6	1239	16	US-10-206-677-1	Sequence 1, Appli
6	1078	77.6	1239	18	US-10-679-813-9	Sequence 9, Appli
7	1047.2	75.3	2040	10	US-09-876-252-129	Sequence 129, App
8	1047.2	75.3	2040	17	US-10-417-820A-129	Sequence 129, App
9	1047.2	75.3	2040	18	US-10-723-955-129	Sequence 129, App
10	1040.8	74.9	2040	17	US-10-417-820A-151	Sequence 151, App
11	501.2	36.1	1179	18	US-10-363-345A-33737	Sequence 33737, A



601 CCTCTCGGCTGTCGCCGCTCTCTGCTCTCGCGGCGCCACCGCGCTCCCGCGCTCG 660  
661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTACCGCGGAATGCGCGCCGAGCCCGCG 720  
661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTACCGCGGAATGCGCGCCGAGCCCGCG 720  
721 CAGCTGGGCGCGCTCGCTGTCATGCTGGGTCACACCGGCTACTTCTTCTGCGCTTT 780  
721 CAGCTGGGCGCGCTCGCTGTCATGCTGGGTCACACCGGCTACTTCTTCTGCGCTTT 780  
781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCG 840  
781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCGCG 840  
841 CTGCGAGCGCGCGCTCGGCGGAGAGAGCGCCACCGCGACCGCTCGGCTCTG 900  
841 CTGCGAGCGCGCGCTCGGCGGAGAGAGCGCCACCGCGACCGCTCGGCTCTG 900  
901 CGTAAGTGGAGCGCGCTGGTTCAAGAGACGCTGCTGCAAGTCCGCGCGCGCGGAGC 960  
901 C----- 901  
961 GCGCAACGCTGGGTCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 1020  
902 ----- 901  
1021 TTTCTATTTCGATTCAGCTCCACCGCGCTGGTGGTCTTGGCATTTATAATTG 1080  
902 -----TGGTGGTGGTCTGGCATTTATAATTG 929  
1081 CTGCTGCGCTTCCAGCTTTCAGATCATTTACATAAACAAGAGATTCGCGGATGAT 1140  
930 CTGCTGCGCTTCCAGCTTTCAGATCATTTACATAAACAAGAGATTCGCGGATGAT 989  
1141 GTACTTCTCAGTACTTAAATCATGCTCGCTGCAACTTTTCTATCTGAGGCGATCTAT 1200  
990 GTACTTCTCAGTACTTAAATCATGCTCGCTGCAACTTTTCTATCTGAGGCGATCTAT 1049  
1201 CAACCAATCTCTAACAACCTCATTTCAAGAGATGACAGCGCGCGCTTTAAACTGCT 1260  
1050 CAACCAATCTCTAACAACCTCATTTCAAGAGATGACAGCGCGCGCTTTAAACTGCT 1109  
1261 GCTCGCAAGAGTCCAGCGCGAGAGGCTTCCACAGAGCAGGACACTGCGGGGAGT 1320  
1110 GCTCGCAAGAGTCCAGCGCGAGAGGCTTCCACAGAGCAGGACACTGCGGGGAGT 1169  
1321 TGCAGGACACTGAGAGACACGCTGGGCTACACCGAGACAGCGCTAACGTGAAGAC 1380  
1170 TGCAGGAGACACTGAGAGACACGCTGGGCTACACCGAGACAGCGCTAACGTGAAGAC 1229  
1381 GATGGGATAA 1390  
1230 GATGGGATAA 1239

RESULT 3  
US-10-290-078-13  
; Sequence 13, Application US/10290078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Cartoll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874  
; FILE REFERENCE: MPI2001-288P1(M)  
; CURRENT FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1239  
; TYPE: DNA

; ORGANISM: Homo Sapien  
US-10-290-078-13  
Query Match 77.6%; Score 1078; DB 15; Length 1239;  
Best Local Similarity 89.1%; Pred. No. 1.9e-281;  
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;  
Qy 1 ATGGGCAAGCCCTCGAAGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Db 1 ATGGGCAAGCCCTCGAAGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Qy 61 GCGCTGCGCGCTTCGAGAGCGGCGGCTGCTCGCGCTTCCCTCGGCGCGCTGCTGCGG 120  
Db 61 GCGCTGCGCGCTTCGAGAGCGGCGGCTGCTCGCGCTTCCCTCGGCGCGCTGCTGCGG 120  
Qy 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180  
Db 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180  
Qy 181 ATGCTGATCGGCGCTTACCGGAGCATGCGGACCAACCACTTGTACCTGGGCGAGCATG 240  
Db 181 ATGCTGATCGGCGCTTACCGGAGCATGCGGACCAACCACTTGTACCTGGGCGAGCATG 240  
Qy 241 GCGCTGCGGACCTACTCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 300  
Db 241 GCGCTGCGGACCTACTCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 300  
Qy 301 TCGGCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 360  
Db 301 TCGGCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 360  
Qy 361 TGCACCTACGCAAGCTGCTGCAATGACCGGCTGCAAGCTGCAAGCTGCAAGCTGCAAG 420  
Db 361 TGCACCTACGCAAGCTGCTGCAATGACCGGCTGCAAGCTGCAAGCTGCAAGCTGCAAG 420  
Qy 421 TGCAGCGCGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 421 TGCAGCGCGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Qy 481 GTGCTGTGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 GTGCTGTGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Qy 541 CAGGACCGCGCATCTCCGAGTCCCGGCTCAATGCGCGCGCTCAATGCGCGCGCTCAATG 600  
Db 541 CAGGACCGCGCATCTCCGAGTCCCGGCTCAATGCGCGCGCTCAATGCGCGCGCTCAATG 600  
Qy 601 CCTCTGCGCTGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Db 601 CCTCTGCGCTGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Qy 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTACAGCGCGGAATGCGCGCGGAGCCCGCG 720  
Db 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTACAGCGCGGAATGCGCGCGGAGCCCGCG 720  
Qy 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCGCG 840  
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCGCGCG 840  
Qy 841 CTGCGAGCGCGCGCTCGGCGGAGAGAGCGCCACCGCGACCGCTCGGCTCTG 900  
Db 841 CTGCGAGCGCGCGCTCGGCGGAGAGAGCGCCACCGCGACCGCTCGGCTCTG 900  
Qy 901 CGTAAGTGGAGCGCGCTGGTTCAAGAGACGCTGCTGCAAGTCCGCGCGCGCGGAGC 960  
901 C----- 901  
961 GCGCAACGCTGGGTCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 1020



Qy 1321 TGCAGGACACTGGAGAGACACGGTGGGCTACACCGAGACAGCGCTAAGCTGAGAC 1380  
Db 1170 TGCAGGACACTGGAGAGACACGGTGGGCTACACCGAGACAGCGCTAAGCTGAGAC 1229  
Qy 1381 GATGGATAA 1390  
Db 1230 GATGGATAA 1239

RESULT 5

US-10-206-677-1  
; Sequence 1, Application US/10206677  
; Publication No. US20030186336A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences, Inc.  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; APPLICANT: Kulander, Bruce G.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO  
; FILE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)  
; CURRENT APPLICATION NUMBER: US/10/206,677  
; CURRENT FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/250,251  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,452  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1239  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-206-677-1

Query Match 77.6%; Score 1078; DB 16; Length 1239;  
Best Local Similarity 89.1%; Pred. No. 1.9e-281;  
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

Qy 1 ATGGGACGCCCTTGAACGGAGACGCGCCCGAGGGGGCGCGGAGCCCGCTGGGCC 60  
Db 1 ATGGGACGCCCTTGAACGGAGACGCGCCCGAGGGGGCGCGGAGCCCGCTGGGCC 60  
Qy 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGATGCGG 120  
Db 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGATGCGG 120  
Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Qy 181 ATGCTGATCGGGCGCTACGGGACATGCGGACCAACCACTTGTACTGGGAGCATG 240  
Db 181 ATGCTGATCGGGCGCTACGGGACATGCGGACCAACCACTTGTACTGGGAGCATG 240  
Qy 241 GCGGTGTCGACCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 300  
Db 241 GCGGTGTCGACCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 300  
Qy 301 TCGGGCCCTGGGTTTCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Db 301 TCGGGCCCTGGGTTTCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Qy 361 TGCACCTAGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Db 361 TGCACCTAGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Qy 421 TCGCCCGCGCTCCGCGCGCGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480  
Db 421 TCGCCCGCGCTCCGCGCGCGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480  
Qy 481 GTGCTCTGGGCGCGTGGCGCTGCTCTCTGCGCGCTGCTCTCTGCTGCTGCTGCTGCT 540

RESULT 6

US-10-679-813-9  
; Sequence 9, Application US/10679813  
; Publication No. US2004020866A1  
; GENERAL INFORMATION:  
; APPLICANT: JASPER, STEPHEN R.  
; APPLICANT: SHEPPARD, PAUL O.  
; APPLICANT: BISHOP, PAUL D.  
; APPLICANT: KUIJPER JOSEPH L.

Db 481 GTGCTCTGGGCGCTGGGCGCTGCTCTCTGCGCGTCCCTTCTTGTCTGCTGGGCGTCGAG 540  
Qy 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCACCCGCGGATCGCTCTCTCG 600  
Db 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCACCCGCGGATCGCTCTCTCG 600  
Qy 601 CCTCTGCGCTCTGCTGCGCGCTCTCTGCGGCGGCGCACCGCGCTGCTGCGGCGCTG 660  
Db 601 CCTCTGCGCTCTGCTGCGCGCTCTCTGCGGCGGCGCACCGCGCTGCTGCGGCGCTG 660  
Qy 661 GGGCCGAGACCGCGGAGGCGCGCGCTGTTACGCGCGAATGCGGCGGAGCCCGCGG 720  
Db 661 GGGCCGAGACCGCGGAGGCGCGCGCTGTTACGCGCGAATGCGGCGGAGCCCGCGG 720  
Qy 721 CAGCTGGGCGCGCTGCGCTGCTGCTGCGGCTCAACCGCGCTACTTCTTCTGCGCTTT 780  
Db 721 CAGCTGGGCGCGCTGCGCTGCTGCTGCGGCTCAACCGCGCTACTTCTTCTGCGCTTT 780  
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGAGCAGCGCGGCGG 840  
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGAGCAGCGCGGCGG 840  
Qy 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGGCGCACCGGAGCGCTCGCGGCTCGT 900  
Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGGCGCACCGGAGCGCTCGCGGCTCGT 900  
Qy 901 CGTAAGTGGAGCGCGCTGGTTCCAAAGACGCTGCTGCGGCGCGCGCGCGGAGCC 960  
Db 901 C----- 901  
Qy 961 GCGCAAAAGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 902 ----- 901  
Qy 1021 TTTCTATTTCGATTCCAGCTCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
Db 902 -----TGGTGGTGGTTCCTGGCATTTATAATTG 929  
Qy 1081 CTGTTGCGCTTCCACGTTGGCAGAAATCATTTACATAAAACAGGAAGATTCCGCGATGAT 1140  
Db 930 CTGTTGCGCTTCCACGTTGGCAGAAATCATTTACATAAAACAGGAAGATTCCGCGATGAT 989  
Qy 1141 GTACTTCTCAGTACTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
Db 990 GTACTTCTCAGTACTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049  
Qy 1201 CAACCCAACTCTTACAACTTCAAGAGTACAGAGCGGCGCTTTAACTGCT 1260  
Db 1050 CAACCCAACTCTTACAACTTCAAGAGTACAGAGCGGCGCTTTAACTGCT 1109  
Qy 1261 GCTCGAAGGAGTCCAGGCGGAGGCTTCCAGAGAGGAGGAGCTGCGGGGAGT 1320  
Db 1110 GCTCGAAGGAGTCCAGGCGGAGGCTTCCAGAGAGGAGGAGCTGCGGGGAGT 1169  
Qy 1321 TGCAGGGGACACTGGAGGAGACACGTTGGGCTACACCGAGACAAGCGCTAACTGAGAGAC 1380  
Db 1170 TGCAGGGGACACTGGAGGAGACACGTTGGGCTACACCGAGACAAGCGCTAACTGAGAGAC 1229  
Qy 1381 GATGGATAA 1390  
Db 1230 GATGGATAA 1239

APPLICANT: DEISHER, THERESA A.  
TITLE OF INVENTION: METHODS OF REGULATING BODY WEIGHT

FILE REFERENCE: 02-23

CURRENT APPLICATION NUMBER: US/10/679,813

CURRENT FILING DATE: 2003-10-03

PRIOR APPLICATION NUMBER: 60/416,918

PRIOR FILING DATE: 2002-10-07

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1239

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1239)

US-10-679-813-9

Query Match 77.6%; Score 1078; DB 18; Length 1239;  
Best Local Similarity 89.1%; Pred. No. 1.9e-281;  
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

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QY 1 ATGGGAGCCCTTGAAACGGAGAGCAGCGCCCGAGGGGGCGCGGAGCGCCGCTGGGCC 60
Db 1 ATGGGAGCCCTTGAAACGGAGAGCAGCGCCCGAGGGGGCGCGGAGCGCCGCTGGGCC 60
QY 61 GCGCTGCGCCCTTGAGAGAGCGCGCTGCTCGCCCTTTCCCTGGGGGCGCTGGTGGCG 120
Db 61 GCGCTGCGCCCTTGAGAGAGCGCGCTGCTCGCCCTTTCCCTGGGGGCGCTGGTGGCG 120
QY 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 ATGCTGATGCGGCGCTACCGGAGACATGCGGAGACACCACTTGTATCTGGGAGCATG 240
Db 181 ATGCTGATGCGGCGCTACCGGAGACATGCGGAGACACCACTTGTATCTGGGAGCATG 240
QY 241 GCGGTGTCGACCTACTATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 300
Db 241 GCGGTGTCGACCTACTATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 300
QY 301 TCGCGGCCCTTGGGTGTTGGGCGCGTGTCTGCGCGCTGTCCCTACGTGCGGCGAGGCG 360
Db 301 TCGCGGCCCTTGGGTGTTGGGCGCGTGTCTGCGCGCTGTCCCTACGTGCGGCGAGGCG 360
QY 361 TGCACCTAGCCACCGCTGTCACATGACCGCGCTCAGGTCGAGCGTACCTGGCCATC 420
Db 361 TGCACCTAGCCACCGCTGTCACATGACCGCGCTCAGGTCGAGCGTACCTGGCCATC 420
QY 421 TCGCGCGCGCTCGCGCGCGCTGTTGGTACCGCGCGCGCTCGCGCGCGCTCATCGCT 480
Db 421 TCGCGCGCGCTCGCGCGCGCTGTTGGTACCGCGCGCGCTCGCGCGCGCTCATCGCT 480
QY 481 GTGCTCTGGGCGCTGGCGCTGCTCTGCGCGTCCCTTTCTTTGTTCTGGTGGGCGTGG 540
Db 481 GTGCTCTGGGCGCTGGCGCTGCTCTGCGCGTCCCTTTCTTTGTTCTGGTGGGCGTGG 540
QY 541 CAGGACCCCGGATCTCGTAGTCCCGGCGCTCAATGACCGCGCGGATCGCTTCCTCG 600
Db 541 CAGGACCCCGGATCTCGTAGTCCCGGCGCTCAATGACCGCGCGGATCGCTTCCTCG 600
QY 601 CCTCTCGCTCGCTCGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 CCTCTCGCTCGCTCGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTGACCGCGGATGCGCGCGAGCGCCGCG 720
Db 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTGACCGCGGATGCGCGCGAGCGCCGCG 720
QY 721 CAGCTGGGCGCGCTCGGTGCTATGCTGTTGGGTACACCGGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGCGCTCGGTGCTATGCTGTTGGGTACACCGGCTACTTCTTCTGCGCTTT 780
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QY 781 CTGTGCTTCAGCATCTCTACGGGCTCATCGGGGGGAGCTGTGAGCAGCCGCGGCGG 840
Db 781 CTGTGCTTCAGCATCTCTACGGGCTCATCGGGGGGAGCTGTGAGCAGCCGCGGCGG 840
QY 841 CTGCGAGGCGCGCGCGCTCGGGGGGAGAGAGCCACCGGCGAGACCGCTCCGCGTCTG 900
Db 841 CTGCGAGGCGCGCGCGCTCGGGGGGAGAGAGCCACCGGCGAGACCGCTCCGCGTCTG 900
QY 901 CGTAAGTGGAGCGCGCTGTGTTCCAAAGACCGCTGCTGAGTCCGCCCGCGCGGGGACC 960
Db 901 C----- 901
QY 961 GCGCAAGCGTGGGTCCCTTCCCTGCTGCGCCAGCTGCTGGGCGCGCTTCCAGTCCC 1020
Db 902 ----- 901
QY 1021 TTTCCTATTTCCGATTCAGCCTCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 902 -----TGGTGGTGGTCTGCGCATTTATAATTG 929
QY 1081 CTGTTGCGCTTCACGTTGGCAGATCATTTACATAAACACGGAAGATTTCGCGGATGAT 1140
Db 930 CTGTTGCGCTTCACGTTGGCAGATCATTTACATAAACACGGAAGATTTCGCGGATGAT 989
QY 1141 GTACTTCTCTCAGTACTTTAAACATCGTCTGCAACTTTTCTATCTGAGCGCATCTAT 1200
Db 990 GTACTTCTCTCAGTACTTTAAACATCGTCTGCAACTTTTCTATCTGAGCGCATCTAT 1049
QY 1201 CAACCCCAATCTCTACAACTCATTTCAAAGAAGTACAGAGCGCGCGCTTTAAACTGCT 1260
Db 1050 CAACCCCAATCTCTACAACTCATTTCAAAGAAGTACAGAGCGCGCGCTTTAAACTGCT 1109
QY 1261 GCTCGAAGGAAGTTCAGGCGGAGAGGCTTCCACAGAAGCAGGAGGAGTCTGCGGGGAGT 1320
Db 1110 GCTCGAAGGAAGTTCAGGCGGAGAGGCTTCCACAGAAGCAGGAGGAGTCTGCGGGGAGT 1169
QY 1321 TGCAGGCGACACTCGAGGAGACACGCTGGGCTACCCGAGACAGCGCTAACGTTGAAGAC 1380
Db 1170 TGCAGGCGACACTCGAGGAGACACGCTGGGCTACCCGAGACAGCGCTAACGTTGAAGAC 1229
QY 1381 GATGGGATAA 1390
Db 1230 GATGGGATAA 1239
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## RESULT 7

US-09-876-252-129

; Sequence 129, Application US/09876252

; Publication No. US20030018182A1

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Lin, I-Lin

; APPLICANT: Dang, Huong T.

; APPLICANT: Chen, Ruoping

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rec

; FILE REFERENCE: AREN-0054

; CURRENT APPLICATION NUMBER: US/09/876,252

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: 09/416,760

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: 60/110,060

; PRIOR FILING DATE: 1998-11-27

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,852

; PRIOR FILING DATE: 1999-02-26



Qy	1	ATGGGCACCCCTTGAAACGGCAGACGACGGCCCGAGGGGGCGCGGGAGCCCGCGGTGGCCC	60
Db	1	ATGGGCAGCCCTTGAAACGGCAGACGACGGCCCGAGGGGGCGCGGGAGCCCGGTGGCCC	60
Qy	61	CGCTGCGCGCTTGGACGAGGGCGCTGTCGCCCTTTCCCTGGGGGGCGCTGGTCCG	120
Db	61	CGCTGCGCGCTTGGACGAGCGCGCTGCTCGCCCTTTCCCTGGGGGGCGCTGGTCCG	120
Qy	121	GTGACCGCTGTGTGCTGTGCTGTGTCGTCTGCGGGGTGAGCGGCAACGTGGTGACCCGTG	180
Db	121	GTGACCGCTGTGTGCTGTGCTGTGTCGTCTGCGGGGTGAGCGGCAACGTGGTGACCCGTG	180

; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled



QY	841	CTGCGAGGCGCGCGCCCTCTGGGGCGGAGAGAGGCCACCGGAGACCGTCCCGCTCCTG	900
Db	841	CTGCGAGGCGCGCGCCCTCTGGGGCGGAGAGAGGCCACCGGAGACCGTCCCGCTCCTG <td>900</td>	900
QY	901	CGTAACTGGAGCGCGCGTGGTTTCCAAAGACGCTGCTGCAGTCCGCGCCCGCGGGAGCC	960
Db	901	CGTAACTGGAGCGCGCGTGGTTTCCAAAGACGCTGCTGCAGTCCGCGCCCGCGGGAGCC	960
QY	961	GGCGAAACGCTGGGTCCCTTCCCTTGCTGGCCCAAGCTCTTGGCGCGCGCTTCCAGTCCC	1020
Db	961	GGCGAAACGCTGGGTCCCTTCCCTTGCTGGCCCAAGCTCTTGGCGCGCGCTTCCAGTCCC	1020
QY	1021	TTTCTCTATTTCGATTCAGGCTCCACCGCGC	1052
Db	1021	TTTCTCTATTTCGATTCAGGCTCCACCGCGC	1052
RESULT 10			
US-10-417-820A-151			
; Sequence 151, Application US/10417820A			
; Publication No. US20030229216A1			
; GENERAL INFORMATION:			
; APPLICANT: Chen, Ruoping			
; APPLICANT: Liaw, Chen W.			
; APPLICANT: Lowitz, Kevin			
; APPLICANT: Chalmers, Derek T.			
; APPLICANT: Behan, Dominic P.			
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled			
; TITLE OF INVENTION: Receptors			
; FILE REFERENCE: 7.US28.CON			
; CURRENT APPLICATION NUMBER: US/10/417,820A			
; CURRENT FILING DATE: 2003-04-16			
; PRIOR APPLICATION NUMBER: 09/416,760			
; PRIOR FILING DATE: 1999-10-12			
; PRIOR APPLICATION NUMBER: 09/170,496			
; PRIOR FILING DATE: 1998-10-13			
; PRIOR APPLICATION NUMBER: 60/110,060			
; PRIOR FILING DATE: 1998-11-27			
; PRIOR APPLICATION NUMBER: 60/120,416			
; PRIOR FILING DATE: 1999-02-16			
; PRIOR APPLICATION NUMBER: 60/121,852			
; PRIOR FILING DATE: 1999-02-26			
; PRIOR APPLICATION NUMBER: 60/109,213			
; PRIOR FILING DATE: 1998-11-20			
; PRIOR APPLICATION NUMBER: 60/123,944			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: 60/123,945			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: 60/123,948			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: 60/123,951			
; PRIOR FILING DATE: 1999-03-12			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 155			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 151			
; LENGTH: 2040			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-417-820A-151			
Query Match 74.9%; Score 1040.8; DB 17; Length 2040;			
Best Local Similarity 99.3%; Pred.No. 2.4e-271;			
Matches 1045; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
QY	1	ATGGGCGAGCCCTTGGAAACGCGACGCGCGCGGAGGGGCGCGGAGCGCGCGCTGCGCCCTTCCCTTGGGGCGCTGGTCCG	60
Db	1	ATGGGCGAGCCCTTGGAAACGCGACGCGCGCGGAGGGGCGCGGAGCGCGCGCTGCGCCCTTCCCTTGGGGCGCTGGTCCG	60
QY	61	GGCTCGCGCTTTCGACAGCGCGCTGCTGCGCCCTTCCCTTGGGGCGCTGGTCCG	120
Db	61	GGCTCGCGCTTTCGACAGCGCGCGCTGCTGCGCCCTTCCCTTGGGGCGCTGGTCCG	120



Query Match	36.1%	Score 501.2	DB 18	Length 1179
Best Local Similarity	79.9%	Pred. No. 2.2e-125		
Matches 590	Conservative 0	Mismatches 148	Indels 0	Gaps 0
QY	1	ATGGGACGCCCTGGAACGGCAGCGCGCCCGAGGGGGCGGGAGCGCGCTGGCCC	60	
DB	442	ATAAACACCCCTAAACAGCAACGACGCGCCCGGAAAAAAGCGGAAACCGCCGTAAACC	501	
QY	61	CGCTGCGCGCTTCGACAGCGCGCGTGTTCGCCCTTTCCTTCGGGGCGCTGGTCGC	120	
DB	502	CGGCTACCGCTTACGACGACGCGCTACTTCGCCCTTTCCTTCGAAACGCTAATACCG	561	
QY	121	GTGACCGCTGTGTCCTGTGCTGCTTCGTCGGGTGAGCGGAGACGTGGTGACCGTG	180	
DB	562	ATACCGCTATATACCTATACCTATTCGTGTCGAAATAAACGACCAACGTAATACCGTA	621	
QY	181	ATGCTGATCGGCGCTACCGGGACATCGGACACCAACCACTTGTACTCTGGGAGCAGATG	240	
DB	622	ATACTAATCGAACGCTACCGAAACATAGAACACCACTTATACCTAAACAAACATA	681	
QY	241	CGCGTTCGACCTACTCATCTCTCGGGTGCCTGTTCGACCTGTACCGCTCTTGGCGC	300	
DB	682	ACCGTATCGACCTACTCATCTACTCGAACTACCGTTCGACCTATACCGCTCTAAGC	741	
QY	301	TCGGCGCCCTGGGGTTCGGGCGCTGCTCTGCGCGCTGTCCCTCTACGTGGGCGAGGCG	360	
DB	742	TCGGACCCCTAAATATTGCAACCGCTACTCTACCGCGCTATCCCTCTACGTAAACGAAAC	801	
QY	361	TGACCTTACGCGACGCTGTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTGGCCATC	420	
DB	802	TACACCTTACGCGACGCTACTACATACCGCGCTCAACGTCTGAAACGCTACTCAACCATC	861	
QY	421	TGCGCGCCGCTTCGCGCGCGCTCTTGGTCAACCGCGCGCGCTCGCGCTCATCGCT	480	
DB	862	TACCGCGCGCTTCGCGCGCGCTCTTAATCACCCGACGCGCGCTCATCGCT	921	
QY	481	GTGCTCTGGGCGGTGGGCGTGTCTCTGCGCGTCCCTTCTTGTTCCTGGTGGGCGTCAAG	540	
DB	922	ATACTCTAAACCGGTAAAGCTACTCTCTACCGATCCCTTCTTATTCCTAATAAAGGTGAA	981	
QY	541	CAGAACCCCGCATCTCCGTAGTCCCGGCGCTCAATGGCACCGCGCGGATCGCTCTCTCG	600	
DB	982	CAAAACCCCGACATCTCCGTAAATCCCGAACCTCAATTAACCGCGCGGAAATCGCTCTCTCG	1041	
QY	601	CCTCTCGCTCTGTCCGCGCTCTCTGTGCTCTCGGGGCGCCACCGCGCTTCCCGCGCGTCG	660	
DB	1042	CCTCTCGCTCTGTCCGCGCTCTCTTAATCTCGGAACGCGCACCGCGCTCCCGCGCTCG	1101	
QY	661	GGGCGCGAGACCGCGGAGCGCGCGCTGTTCAGCGCGGAATCGCGGCGAGCCCGCGCG	720	
DB	1102	AAACCCGAAACCGCGAAACCGGACGCTATTTCACCGGGAATACGACCGAAACCGCGCG	1161	

Query Match	36.1%	Score	501.2	DB	19	Length	1179
Best Local Similarity	79.9%	Pred. No.	2.2e-125				
Matches	590	Conservative	0	Mismatches	148	Indels	0
QY	1	ATGGGACGCCCTTGGAAACGCGACGCGCCCGAGGGGGCGCGGAGCGCGCTGGGCC	60				
DB	738	ATAAAACAAACCCCTAAACACGACACGACCGCCCGAAAAACGGAACACGCGCTAACCC	679				
QY	61	GCCTCGCGCCTTGGACAGAGCGCGCTGTCTGCGCCTTTTCCCTTGGGGGCGCTGGTGC	120				
DB	678	GCCTACTACGCGCTTACGACGAACGCGCTACTCGCGCTTTCCCTTAAAAACGCTAATAC	619				
QY	121	GTGACCGCTGTGTCCTGTGTCCTGTTGCTGCTCGGGGTGACGCGCAACGTGGTGACCGGT	180				
DB	618	ATAACCGCTATATACCTATATACCTATTTCGTCTGAAATAACGACAACGTAAATAACCGTA	559				
QY	181	ATGCTGATCGGGCGCTACCGGGACATGCGGACCAACCAACTTTGTACTTGGGACGATG	240				
DB	558	ATACTAATGAACGCTACCGAAACATACGAACCAACCAACCAACTTTATACCTAAACAACATA	499				
QY	241	GCGGTGCGGACCTACTCATCTCTGCTCGGGCTGCGGTTGCACTGTACCGCTCTGGGCG	300				
DB	498	ACGCTATCGACCTACTCATCTCTCGAACTACCGGTTGCACTGTACCGCTCTTAACGC	439				
QY	301	TCGCGGCCCTTGGGTGTTTGGGGCGCTGCTCTGCGCGCTGTCCCTCTACGTGGGCGAGGC	360				
DB	438	TCGCGACCTTAATATTCGAAACGCTACTCTACGCGCTATCCCTCTACGTAAACGAAAC	379				
QY	361	TGCACTAGCCACGCTGTGCAATGACCGCGCTCAGCTCGAGCGCTACCTGGCCATC	420				
DB	378	TACACCTAGCCACGCTACTTACACATAAACCGCGCTCAACGTCGAACGCTACTTAACCATC	319				
QY	421	TGCGCGCGCTCGCGCGCGCTTGGTTCACCGGCGCGGTCGCGGCGCTCATCGCT	480				
DB	318	TACCGCGCGCTCGCGCGCGCGCTTAAATCACCGACGCGCGCTCGCGGCGCTCATCGCT	259				
QY	481	GTGCTCTGGGCGCTGGCGCTGCTCTCTGCGCGTCCCTTTTGTTCCTGTGGGCGCTCGAG	540				
DB	258	ATACTCTAACCGTAAGCGTACTCTCTACGATCCCTTCTATTTCCTAATAAACGTCGAA	199				
QY	541	CAGAACCCGGGATCTCCGTAGTCCGGGCGCTCAATGGGCAACGGCGCGGATCGCCCTCTCG	600				
DB	198	CAAAACCCCGACATCTCGTAATCCGGAACCTCAATAACACCGCGCGAATCGCTCTCTCG	139				

QY 601 CCTCTCGCTCGTCCCGCCCTCTCTGGCTTCGCGGGGCCACCCCGTCCCGCGCTCG 660  
Db 138 CCTCTCGCTCGTCCCGCCCTCTCTAACTCTCGGAAACGCCACCGCTCCCGCGCTCG 79  
QY 661 GGGCCCGAGACCGCGGAGCCCGCGCTGTTCAGCCCGGATGCGGCCGAGCCCGCG 720  
Db 78 AAACCCGAAACCGCGAAACCGCGAGCTATTCAACCGCGAATACCGACCGAAACCCCG 19  
QY 721 CAGCTGGGCGCGCTCGT 738  
Db 18 CAACTAAACGCGCTACGT 1  
RESULT 14  
US-10-363-483A-33738  
; Sequence 33738, Application US/10363483A  
; Publication No. US20050064401A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain  
; TITLE OF INVENTION: illnesses  
; FILE REFERENCE: 82011  
; CURRENT APPLICATION NUMBER: US/10/363,483A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 33738  
; LENGTH: 1179  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: Cpg-island No: 33738  
US-10-363-483A-33738

Query Match 36.1%; Score 501.2; DB 19; Length 1179;  
Best Local Similarity 79.9%; Pred. No. 2.2e-125;  
Matches 590; Conservative 0; Mismatches 148; Indels 0; Gaps 0;  
QY 1 ATGGCAGCCCTTGAACGGGAGCAGCGCCCGGAGGGGGCGCGGAGCCCGCTGGGCC 60  
Db 442 ATAAACAACCCCTTAAACGACAAACGACCGCCCGGAAAAACCGAAACCCCGTAAACC 501  
QY 61 GGGCTGCGCCCTTGGCAGGCGCGCTGCTCGCCCTTCCCTGGGGCGCTGGTGCG 120  
Db 502 GGGCTACCGCTTAGCAGAAACCGCTACTCGCCCTTCCCTTAAACGCTAATACG 561  
QY 121 GTGACCGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
Db 562 ATAAACCGCTATATACCTATACCTATTCTGTGCTGAAATAAAGCAACGTAATACCGTA 621  
QY 181 ATGCTGATCGGGCTACCGGACATGCGGACACCAACCACTTGTACTGGGAGCATG 240  
Db 622 ATACTAATCGAACGCTTACCGAAACATACGAAACCAACCACTTATACCTAAACACATA 681  
QY 241 GCGGTGTCCGACCTACTCATCTGTCTGGGCTGCGGCTTGCACCTGTACCGCTCTGGGCG 300  
Db 682 ACCGTATCGACCTACTCATCTACTCGAACTACCGCTTGCACCTATACCGCTCTAAACG 741  
QY 301 TCGCGCCCTGCGGTGTGCGGCGCTGTCTGCGCCCTGTCCCTCTACGTGGGCGAGGCG 360  
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QY 361 TCGACCTAGCCACGCTGTGACATGACCGGCTCAGGCTCGAGGCTACCTGCGCATC 420  
Db 802 TACACCTAGCCACGCTACTACACATAACCGGCTCAACGCTCGAACGCTTACCTAACCATC 861  
QY 421 TCGCGCCGCTCGCGCCCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 862 TACCGCCGCTCGCGCCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921  
QY 481 GTGCTGTGGGCGGTGGCGCTGTCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

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QY 541 CAGGACCCCGGCATCTCGTAGTCCCGGCTCAATGSCACCGCGGATCGCTCTCTCG 600  
Db 982 CAAAACCCGACATCTCGTAATCCGAACTCAATACACCGCGGATCGCTCTCTCG 1041  
QY 601 CCTCTCGCTCGTCCCGCTCTCTCTGCTTCGCGGGCGCACCGCTCCCGCGCTCG 660  
Db 1042 CCTCTCGCTCGTCCCGCTCTCTAACTCTCGGAAACCGCACCGCTCCCGCGCTCG 1101  
QY 661 GGGCCCGAGACCGCGGAGCCCGCGCTGTTCAGCCCGGATGCGGCCGAGCCCGCG 720  
Db 1102 AAACCCGAAACCGCGAAACCGCGAGCTATTCAACCGCGAATACCGACCGAAACCCCG 1161  
QY 721 CAGCTGGGCGCGCTCGT 738  
Db 1162 CAACTAAACGCGCTACGT 1179  
RESULT 15  
US-10-363-345A-33739  
; Sequence 33739, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 33739  
; LENGTH: 1179  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: Cpg-island No: 33739  
US-10-363-345A-33739  
Query Match 31.5%; Score 437.2; DB 18; Length 1179;  
Best Local Similarity 74.5%; Pred. No. 4.5e-108;  
Matches 550; Conservative 0; Mismatches 188; Indels 0; Gaps 0;  
QY 1 ATGGCAGCCCTTGAACGGGAGCAGCGCCCGGAGGGGGCGCGGAGCCCGCTGGGCC 60  
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QY 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180  
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QY 181 ATGCTGATCGGGCGCTACCGGACATGCGGACCAACCACTTGTACTGGGAGCATG 240  
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Db 922 GTGTTTGGGTCGTGGCGTGTGTTTGTGCGGTTTGTGCGGTTTGTGCGGTTTGTGCGGTCGAG 981  
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Db 982 TAGGATTCGGTATTTTCGTAGTTTCGGGTTTAAAGGTATCGCGGATCGTTTTTCG 1041  
QY 601 CCTCTCGCTCTGCGCGCTCTCTGCTCTCGGGGCGCCACCGCGTCCCGCGCTCG 660  
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Search completed: April 11, 2005, 21:00:30  
Job time : 819.545 secs







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 Db 295 GAAACTCTTCCAGTTGTCAGGAGAGCTGACCTAGCCACGCTTCTCACCATCACCG 354  
 Qy 392 CGCTCAGGCTCGAGGCTACCTGGCGATCTGCGCGCGCTCGCGCGCGCTTGGTCA 451  
 Db 355 CGCTGAGCGTTCAGCGCTACTTCGCCATCTGCTTCGCGTGGCGCGAGGTGGTCA 414  
 Qy 452 CCGCGCGCGCTCGCGCGCTCATGCTGCTGCTGCGCGCTGCGCTGCTGCTGCTGCGG 511  
 Db 415 CCAAGGCGCGTGTGAAGCTGCTCATCTTGTCTCATCTGCGCGCTGCGCTTCTGCGCGG 474  
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 Db 475 GCGCCATCTTCTGCTGCTGCGGCTGCGAGGACGAGAACCGCA 516

RESULT 2  
 LOCUS AK049671  
 DEFINITION Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone: C530020122 product: GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 homolog [Rattus norvegicus], full insert sequence.  
 ACCESSION AK049671  
 VERSION AK049671.1 GI:26340405  
 KEYWORDS HTc; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 Carninci, P. and Hayashizaki, Y.  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 4  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED

AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
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 AUTHORS  
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 REFERENCE  
 FEATURES  
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 CDS  
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 Query Match  
 Best Local Similarity  
 Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;  
 Qy 92 CGCCCTTCCCTCGGGCGCTGTCGCGGTGACCGCTGTCGCTGTCGCTGTCGTCG 151

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 4435)  
 Fukuda, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Adachi, J., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
 Location/Qualifiers  
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 Best Local Similarity 68.6%; Pred. No. 1.8e-38;  
 Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;  
 Qy 92 CGCCCTTCCCTCGGGCGCTGTCGCGGTGACCGCTGTCGCTGTCGCTGTCGTCG 151

355	Db	CACTGTTCCCGGCGCTGCTGGCGGCGTCATGCCACCTGCGTGGCGCTCTTGGTG	414
152	Qy	TGCGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGCGCTACCGGACATCGGA	211
415	Db	TGGGCATCTCGGCAACCTGCTCACCATGCTGGTGGTCCCGCTTCGGCGAGCTGGCA	474
212	Qy	CCACCAACCAACTGTACTCGGCAAGCATGGCCGTTCGACCTACTCATCTCTCGGAC	271
475	Db	CCACCACCAACCTCTACCTATCCAGCATGGCCTTCGGAATCTGCTCATCTCTGTGCA	534
272	Qy	TGCGGTTGCAACCTGTACCGCTCTGGCGCTCGCGGCCCTGGGTGTTGGGCGCGCTGCT	331
535	Db	TGCGCTGGACCTCGTCCGCGCTCTGGCAGTATCGGCCCTGGAACTTCGGCGACCTGCT	594
332	Qy	GCGCGCTGCTCTACTGTTGGCGAGGCTGCACCTAGCCACGCTGCTGCACATCAGCG	391
595	Db	GCAACTCTTCAGTTTGTACGAGAGAGCTGCACCTACGCCAGGTCCTCACCATCAGCG	654
392	Qy	CGCTCAGCGTCGAGCGCTACTGGGCATCTGCGCGCGCGCTCCGCGCCGCGTCTTGCTCA	451
655	Db	CGCTGAGCGTCGAGCGCTACTTCGGCATCTGCTTCGCGCTCGGGCCAGGTGGTGTCA	714
452	Qy	CCGCGCGCGCTCGCGCGCTCATCGTGTGCTCTGGCGCGTGGCGCTGCTCTCTGCGG	511
715	Db	CCAAGGCGCTGGAAGCTGGTTCATCTCTTGTCAATTTGGCGCGTGGCCTCTCTGCAGCGG	774
512	Qy	GTCCCTTCTTGTCTCGTGGGCTCGAGCAGACCCCGGCA	553
775	Db	GGCCATCTTTCGTGTGGCGGTGGAGCAGGAGACCGCA	816

RESULT 3					
C0959476					
LOCUS	C0959476	688 bp	mRNA	linear	EST 17-AUG-2004
DEFINITION	AGENCOURT 30842629 NIH_MGC_146 Homo sapiens cDNA clone				
	IMAGE:7389798 5', mRNA sequence.				

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ACCESSION      CO959476
VERSION        CO959476.1  GI:51324050
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1 (bases 1 to 688)
               NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Daniela S. Gerhard, Ph.D.
               Office of Cancer Genomics
               National Cancer Institute / NIH
               Bldg. 31 Rm10A07 Bethesda, MD 20892
               Email: cgapbs@mail.nih.gov
               Tissue Procurement: Guthrie cDNA Resource Center
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: IRBi8 row: c column: 04
               High quality sequence stop: 170.
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                   /clone_lib="NIH MGC 146"
                   /note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
                   multiple; ORF's were PCR-amplified (from IMAGE Clones or

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from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center ([www.guthrie.org/cDNA](http://www.guthrie.org/cDNA)) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file [http://image.llnl.gov/image.rearrayed/plates/IRBF\\_presv.dat](http://image.llnl.gov/image.rearrayed/plates/IRBF_presv.dat) as a Note: this is a NIH MGC Library."

## ORIGIN

Query Match	16.4%;	Score 228.4;	DB 7;	Length 688;
Best Local Similarity	79.8%;	Pred. No. 3.6e-38;		
Matches 265;	Conservative 0;	Mismatches 67;	Indels 0;	Gaps 0;
QY	1	ATGGGCAGCCCTTGGAAACGCGACGACGGCCCGAGGGGCGCGGGAGCCGCGTGGCCCC	60	
Db	3	ATGGGCAGCCCTTGGAAACGCGACGACGGCCCGAGGGGCGCGGGAGCCGCGTGGCCCC	62	
QY	61	GCCTCTCGCGCTTTGCGACGAGCGCCGCTGCTCGCCCTTTCCTTGGGGGCGCTGGTGCCG	120	
Db	63	GCCTCTCGCGCTTTGCGACGAGCGCCGCTGCTCGCCCTTTCCTTGGGGGCGCTGGTGCCG	122	
QY	121	GTGACCGCTGTGTGCTGTGCTTTCGTCGTGCGGGGTGACGGGCAACGTGTGTGACCGTG	180	
Db	123	GTGACCGCTGTGTGCTGTGCTTTCGTCGTGCGGGGTGTGCGGTTCGTGTGTGTCGCG	182	
QY	181	ATGCTGATCGGGCGCTACCGGGACATGCGGACACACCAACTGTACCTGGCGCAGCATG	240	
Db	183	TTGTTGCTCTGGCGCTGTGCGGNGTTGTGGGGCTCTTCTCTTGGCCCTTGGGGCGCGCG	242	
QY	241	CGCGTGTCCGACCTACTCATCTCGTCCGGCTGCCGTTCGACCTGTACCCGCTCTTGGCGC	300	
Db	243	TGGGTGCTGNNNGTCTCTCCCGTTTNGCCNGGGTGGCGGTGTCGGCCCTTGGCTC	302	
QY	301	TCGCGGCCCTTGGGTGTTCGGGCCGCTGCTGTG	332	
Db	303	TCGCTGGCNGTGTGTGTTCCGGGTGTGCTTGG	334	

## RESULT 4

LOCUS	CD618070	640 bp	mRNA	linear	EST 12-JAN-2004
DEFINITION	5603036.H1 FLP Homo sapiens cDNA, mRNA sequence.				
ACCESSION	CD618070				
VERSION	CD618070.1	GI:40266335			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 640)				
TITLE	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes				
JOURNAL	Genomics 84 (1), 205-210 (2004)				
COMMENT	Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com. Location/Qualifiers 1..640				
FEATURES					
SOURCE					

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/organism="Homo sapiens"
/mol_type="mRNA"
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## ORIGIN

Query Match 16.4%; Score 227.8; DB 6; Length 640;  
Best Local Similarity 68.3%; Pred. No. 4.8e-38;  
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 93 GGCCTTTCCTCGGGCGCTGCTGCGGTGACGCTGTGTGCTGTGCTGTTCGTCTGT 152

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481 GCTCTTCCCGCGCGCTGCTGGCGGGGCTCACAGCCACCTTCGCTGGT 422
153 CGGGGTAGCGGCAACGTTGACCGTATCGGGCGCTACCGGACATCGGAC 212
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213 CACCACCAACTTGTACTCTGGGAGAGTGGCGGTGTCGACCTACCTATCTCTGGTGGCT 272
361 CACCACCAACTTGTACTCTGGGAGAGTGGCGGTGTCGACCTACCTATCTCTGGTGGCT 302
273 GCGGTTCGACCTGTACCGCTCTGCGCTCGCGGCTTCGGGTGTTTCGGGCGCTGCTCTG 332
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121 CAAAGGCGGGTGAAGCTGGTTCATCTGCTATCTGGCGCGTGGCTCTGCGAGCGCG 62
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61 GCCCATCTTCGTGCTAGTTCGGGTGGAGCAGAGAACGGCACC 19

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RESULT 5
LOCUS CD618071 640 bp mRNA linear EST 12-JAN-2004
DEFINITION CD618071 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD618071
VERSION CD618071.1 GI:40266336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 640)
AUTHORS Fu G.K., Wang J.T., Yang J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 16.4%; Score 227.8; DB 6; Length 640;
Best Local Similarity 68.3%; Pred. No. 4.8e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 93 GCCCTTTCCCTGGGGCGCTGTTGCGGCTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGT 152
DB 157 GCTCTTCCCGCGCGCTGCTGCGGGGCTGACAGCCACCTTCGTTGGCCTCTCTGTTGT 216
QY 153 CGGGGTAGCGGCAACGTTGACCGTATGCTGATCGGGCGCTACCGGCGCATCGGAC 212
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QY 213 CACCACCAACTTGTACTCTGGGAGAGTGGCGGTGTCGACCTACTCATCTCTGCTCGGGCT 272
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QY 273 GCGGTTGACGCTGTACCGCTCTGCGGCTCGCGGCTTCGGGTGTTTCGGGCGCTGCTCTG 332
DB 337 GCGGCTGACCTCTGTTGCGCTCTGCGAGTACCGGCGCTTGGAACTTCGGGCGACCTCTCTG 396
QY 333 CCGGCTGCTCTTACCTGGGCGAGGCTGCACCTACCGCAGCGCTGTCGACATGACCGC 392
DB 397 CAAACTCTTCCAACTTCGTAGTGGAGCTGACCTACCGCAGGCTGCTCACCATCACAGC 456
QY 393 GCTCAGGCTTCGAGCGCTACCTGGGCTCTGCGGCGCTTCGGCGCGCTTCCTTGGTTCAC 452
DB 457 GCTGAGCGTTCGAGCGCTACTTTCGCCATCTGCTTCCCACTTCGGGCGCAAGTGGTGTCTAC 516
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RESULT 6
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DEFINITION Homo sapiens GHBR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407664
VERSION AY407664.1 GI:39763635
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1052)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1052)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 68.3%; Pred. No. 4.9e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 93 GCCCTTTCCCTGGGGCGCTGTTGCGGCTGACCGCTGTGCTGTGCTGTGCTGTGCTGT 152

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119	GGGTATCGCTGGCAACCTGCTCACCATGCTGGTGTGCGCTTCGCGAGCTCGGCAC	178
213	CACCACAACTTTGATCTGGGCGAGATGGCGGTGCCGACCTACTCATCTCTCGGCGT	272
179	CACCACAACTCTACTGCTCCAGCATGGCTTCTCCGATCTGCTCATCTTCTCTGTGAT	238
273	GCCGTTTCGACCTGTACCGCCTCTGCGCTCTCGCGCCCTGGGTGTTCCGGCGCGTCTCTGT	332
239	GCCCTTGAACCTCGTTCCGCTTGGCAGTACGCGCCCTGGAACTTCGGGGAACCTCTCTGT	298
333	CGGCTGTCTCTTACGTGGGCGAGGGGTGCACCTACGCCACGTGCTGCACATGACCGC	392
299	CAAACTCTTCCAAATTCGTTCAGTGAGAGCTGCACCTACGCCACGGTGTCAACCATCACAGC	358
393	GCTCAGGTCGAGCGCTACCTGGCCACTGCGCGCGCTCCGCGCCCGCGCTTTGGTCAC	452
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453	CCGGCGCGCGCTCCGCGGCTCATCGCTGTGCTCTGGGGCCGTGGCGGCTCTCTTCGCGGG	512
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RESULT 7  
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LOCUS BF603623 500 bp mRNA linear EST 25-APR-2001  
DEFINITION 289181 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION	BF603623	
VERSION	BF603623.1	GI:11701421
KEYWORDS	EST.	
SOURCE	Bos taurus	
ORGANISM	Bos taurus (cow)	
REFERENCE	1 (bases 1 to 500)	
AUTHORS	Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keefe, J. W.	
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	
JOURNAL	Genome Res. 11 (4), 626-630 (2001)	
MEDLINE	21180013	
PUBMED	11282978	

COMMENT

Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred  
v.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.

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FEATURES             source
PCR Primers
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  BACKWARD: GTTTCCTCAGTCACGACG
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              /mol_type="mRNA"
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		/clone_lib="MARC 3BOV"	
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		Library made from pooled tissue from marrow, alveolar	
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		longissimus muscle."	
ORIGIN			
Query Match		16.3%; Score 226.8; DB 2; Length 500;	
Best Local Similarity		68.2%; Pred. No. 7.7e-38;	
Matches 315; Conservative		0; Mismatches 147; Indels 0; Gaps 0;	
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Qy	152	TCGGGTGAGCGCAACGTGTGACCGTGATGTGATTCGGGGCGCTACCGGGACATGCGGA	211
Db	99	TGGGCATTCGGGGCAACCTGCTCACCATGTGTGTGTGTGTCGCGTTTCCGCGAGCTGGGTA	158
Qy	212	CCACCACCAACTTGTAACCTGGGGCAGATGCCGTGTCCGACCTTACTCATCTCTGTGGGC	271
Db	159	CGACCAACCAACTCTTACCTGTGCAGATGGCCCTTCTCCGACTTACTCATCTTCTCTGCA	218
Qy	272	TGCGGTTCGACCTGTACCGCCTCTGGCGCTTCGGCGCCTGGGGTTCGGGCGCGTGTCT	331
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Qy	332	GCCGCTGTCCCTCTACGTGGGGAGGGCTGACCTTACGCCACGCTGCTGCACATGACCG	391
Db	279	GCAACTCTTCAGTTTGTACGAGAGCTGCACCTTACGCTACGGTGTCTCACCATACCG	338
Qy	392	CGCTACGCTGAGCGCTACTCTGGCCATCTGCCGCCGTCTCGCGCCCGCTTTGGTCA	451
Db	339	CGCTGAGCGTCAAGCGCTACTTCCCATCTCTCTTCCTCGCTCGCGGGCAAGTGGTGATCA	398
Qy	452	CCGGCGCGCGTCCGCGCGCTCATCGCTGTCTCTGGGCGGGGGCGCTCTCTCTGCCG	511
Db	399	CCAAGGCGGGTGAAGCTGTATCTGGTCACTTGGGGCGTGGCTTCTGAGCGCG	458
Qy	512	GTCCCTCTTTGTTCTGTGGGGCGTGCAGACGACCCCGCA	553
Db	459	GGCCCATCTTCGTGCTGTGTGGAGTGGAGCATCAGAAATGGCA	500

RESULT 8					
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LOCUS	CD618076	637 bp	mRNA	linear	
DEFINITION	56030461H1	FLP	Homo sapiens	CDNA, mRNA	sequence.
					EST 12-JAN-2004

CD618076  
CD618076.1 GI:40266341  
EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 637)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
COMMENT Contact: Fu GK

Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.  
 Location/Qualifiers  
     1. .637  
         /organism="Homo sapiens"  
         /mol\_type="mRNA"  
         /db\_xref="taxon:9606"  
         /clone\_lib="FLP"  
 FEATURES  
     source



## FLC I."

ORIGIN

Query Match 15.8%; Score 219.2; DB 6; Length 608;  
 Best Local Similarity 70.3%; Pred. No. 3.2e-36;  
 Matches 293; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 137 TGTGCTCTTGTGTCGGGTGAGCGGACGATGGTGTACCGTGTATGTCATCGGCGCT 196  
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QY 197 ACCGGACATCGGACACCACTTGTACCTGGGAGATGGCGCTGTGCGACCTAC 256  
 Db 62 TCCGGAGCTGCGACACCACTTGTACCTATTCAGATGCGCTTCTCCGATGTC 121

QY 257 TCATCTCTCTGCGGTCTGCACTGTATACCGCTCTGCGCTCTGCGGCTTGGGTGT 316  
 Db 122 TCATCTCTCTGCGGTCTGCACTGTATACCGCTCTGCGCTCTGCGGCTTGGGTGT 181

QY 317 TCGGCGCTGCTTGGCGCTGCTGCTTACGTGGGAGGCTGTACCTACGCGCAGC 376  
 Db 182 TCGGCGCTGCTTGGCGCTGCTGCTTACGTGGGAGGCTGTACCTACGCGCAGC 241

QY 377 TGCTGCATCAGCGCTGAGCGTACCTGCGCTATCTGCGGCTTGGGTGTGCGG 436  
 Db 242 TCCTCACCATCAGCGCTGAGCGTACCTGCGCTATCTGCGGCTTGGGTGTGCGG 301

QY 437 CCGCGCTTGTGCTCAGCGCTGAGCGTACCTGCGCTATCTGCGGCTTGGGTGTGCGG 496  
 Db 302 CCAGGTGCTGCTCAGCGCTGAGCGTACCTGCGCTATCTGCGGCTTGGGTGTGCGG 361

QY 497 CGCTGCTCTGCGGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553  
 Db 362 CTTCTGCGGCGGCGGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418

RESULT 10

LOCUS BF513101

DEFINITION UI-H-BW1-amm-e-07-0-UI.s1 NCI CGAP\_Sub7 Homo sapiens cDNA clone IMAGE:3070549 3', mRNA sequence.

ACCESSION BF513101

VERSION BF513101.1 GI:11598280

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Oligo-dt track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: M13 Forward  
 POLYA=No.

FEATURES

Location/Qualifiers

1..590

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3070549"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP Sub7"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP\_Sub7 is a subtracted library derived from NCI CGAP\_Sub6. The

NCI CGAP Sub7 library had 12 million recombinants. A single-stranded DNA preparation of NCI CGAP\_Sub6 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI CGAP\_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3082-3068 (IMAGE Clones 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clones 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP\_Sub1 (IMAGE Clones 2708616-2710535) and NCI CGAP\_Sub2 (IMAGE Clones 2710536-2712455) (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP\_Sub3 (IMAGE Clones 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP\_Sub4 (IMAGE Clones 2723592-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP\_Sub6 (IMAGE Clones 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG\_SEQ=None found"

## ORIGIN

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QY 895 GTCTGTGCTAGTGGAGCGCGCGTGTTCAGAGCGCTGCTGCGAGTGGCGCGCGG 954  
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QY 955 GGGACCGCGGCGGCGGCGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1014  
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QY 1015 GCTCCCTTCTCTATTTCCAGCTTCCAGCTTCCAGCGCGCGGCGGCGGCGGCGG 1052  
 Db 181 GCTCCCTTCTCTATTTCCAGCTTCCAGCTTCCAGCGCGCGGCGGCGGCGGCGG 218

## RESULT 11

LOCUS AY407665

DEFINITION Pan troglodytes GHSP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY407665

VERSION AY407665.1 GI:39763636

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. (bases 1 to 969)

AUTHORS Clark, A.G., Glanbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous







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XhoI; cDNA made by oligo-dT priming. Directionally cloned  
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GGCAGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH_MGC Library."
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## ORIGIN

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534 GGTGGTTCTGCGATTATAATTGCTGGTGGCTTCCACGTTGGCAGAAATCAATTACAT 593  
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1117 AAACACGGAAGATTCGCGGATGATGACTTCTCTCAGTACTTTAACATCGTCGCTCTGCA 1176  
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594 AAACACGGAAGATTCGCGGATGATGACTTCTCTCAGTACTTTAACATCGTCGCTCTGCA 653  
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1177 ACTTTTCTATCTGAGCGCATCTATCAACCCCAATCCTCTACAACCTCAATTTCAAAGAAGT 1235  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
654 ACTTTTCTATCTGAGCGCATCTATCAACCCCAATCCTCTACAACCTCAATTTCAAAGAAGT 713  
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1236 AC-AGAGCGCGGCTTTTAA-CTGCTGCTCGCAGGAGTCCAGGCGGAG-AGGCT 1289  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
714 ACAAGAGCGGCGGCTTTTAACTGCTGCTCGCAGGAGTCCAGGCGGAGGAGCT 773  
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1290 TCCACAGAGCAGGAGACACTGCGGGG 1316  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
774 CCCACAGAGCAGGAGACACTGCGGGG 800
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Search completed: April 11, 2005, 12:57:52  
Job time : 5513.89 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2005, 12:58:01 ; Search time 64.3333 Seconds  
(without alignments)  
2320.562 Million cell updates/sec

Title: US-09-719-485-5

Perfect score: 2043

Sequence: 1 MGSPWNGSGPEGAREPPW.....WQNLHKRGRFADVDLLSVL 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2043	100.0	386	3	Aay54146 Amino aci
2	2043	100.0	386	4	Aab62653 Short for
3	2043	100.0	386	8	Adn11763 Human mot
4	1581	77.4	412	3	Aay54145 Amino aci
5	1581	77.4	412	4	Aab68478 Amino aci
6	1581	77.4	412	4	Aab62652 Long form
7	1581	77.4	412	5	ABG30936 Human G p
8	1581	77.4	412	5	ABP81993 Human mot
9	1581	77.4	412	8	Adn11761 Human mot
10	1581	77.4	412	8	Ado29697 Human GPC
11	1581	77.4	412	8	Adq37921 Human G-p
12	1581	77.4	501	4	AAG65822 Human GPR
13	1575	77.1	412	3	AAB02854 Human G p
14	1575	77.1	412	8	Adg86491 Human hGP
15	1575	77.1	412	8	Adg86511 Human orp
16	1575	77.1	412	8	Adp20284 Human GPC
17	1575	77.0	412	5	ABs09535 Human mot
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20	1149.5	56.3	271	4	AAB68476 Amino aci
21	673.5	33.0	363	3	AAY54147 The puffed
22	673.5	33.0	363	4	AAB68479 Amino aci
23	649	31.8	289	2	AAW19216 Swine gro
24	649	31.8	289	2	AAW19609 Pig growt
25	649	31.8	289	2	AAW19611 Human gro

26	649	31.8	289	6	ABP81828	Abp81828 Human gro
27	644	31.5	289	2	AAW19218	AAW19218 Human gro
28	644	31.5	349	3	AAy69293	AAy69293 A canine
29	643	31.5	366	3	AAy70345	AAy70345 Human G p
30	643	31.5	366	3	AAy90632	AAy90632 Human G p
31	643	31.5	366	4	AAAB97376	AAAB97376 Rat growt
32	643	31.5	366	4	AAAB62650	AAAB62650 Human G-p
33	643	31.5	366	5	AAAB09534	AAAB09534 Human ghr
34	643	31.5	366	7	ADc22607	ADc22607 Human G p
35	643	31.5	366	7	ADH14080	ADH14080 Human GHS
36	643	31.5	366	8	ADD35398	ADD35398 Human gro
37	643	31.5	366	8	ADN12078	ADN12078 Protein #
38	643	31.5	366	8	ADN11756	ADN11756 Human gro
39	643	31.5	366	8	ADO29025	ADO29025 Human nov
40	643	31.5	366	8	ADQ28857	ADQ28857 Human ghr
41	641	31.4	364	3	AAy54565	AAy54565 A mouse g
42	641	31.4	364	4	AAAB97377	AAAB97377 Rat growt
43	641	31.4	364	8	ADO29026	ADO29026 Mouse nov
44	639.5	31.3	353	2	AAW19215	AAW19215 Swine gro
45	639.5	31.3	353	2	AAW19608	AAW19608 Pig growt

#### ALIGNMENTS

##### RESULT 1

AAy54146  
ID AAY54146 standard; protein; 386 AA.

AC AAY54146;

XX XX 27-MAR-2000 (first entry)

DE Amino acid sequence of the motilin receptor splice variant MTL-R1B.

XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;

KW spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;

KW functional defect; neurological disorder; scleroderma; colonoscopy;

KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;

KW infection; stress-related motility disorder; psychogenic disorder;

KW gastroparesis; gastro-oesophageal reflux disease; constipation;

KW chronic idiopathic pseudo obstruction; acute faecal impaction;

KW postoperative ileus; gallstones; infantile colic; diarrhoea;

KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;

KW endoscopy; duodenal intubation.

XX OS Homo sapiens.

XX PN WO9964436-A1.

XX PD 16-DEC-1999.

XX PF 08-JUN-1999; 99WO-US012773.

XX PR 12-JUN-1998; 98US-0089098P.

XX PA (MERI ) MERCK & CO INC.

XX PI Feighner SD, Patchett AA, Tan C, Mckee K, Macneil D, Howard AD;

XX PI Pong S, Smith RG;

XX DR WPI; 2000-105868/09.

XX DR N-PSDB; AAZ45404.

XX XX Novel receptor protein for screening compounds used in treating irritable

PT bowel syndrome, constipation and other gastric conditions.

XX Claim 5; Fig 5; 44pp; English.

XX CC The present sequence represents splice variant MTL-R1B of the motilin

CC receptor. The gene encodes a G-protein coupled receptor, and is

CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A

CC (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven

transmembrane domain form, and MTL-R1B is a truncated five transmembrane domain. The MTL-R1 proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological disorders e.g. scleroderma, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychogenic disorders, chronic gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathic pseudo obstruction, acute faecal impaction, postoperative ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy, endoscopy and duodenal intubation

Sequence 386 AA;  
Query Match 100.0%; Score 2043; DB 3; Length 386;  
Best Local Similarity 100.0%; Pred. No. 1e-171;  
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60  
1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60  
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120  
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120  
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
181 QDPGISVVPGLNCTARIASSPLASSPPLWLSRAPPSPGPGTAAALFRCRCPSPA 240  
181 QDPGISVVPGLNCTARIASSPLASSPPLWLSRAPPSPGPGTAAALFRCRCPSPA 240  
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300  
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300  
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360  
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360  
361 LVALPRWQNLHKGHRFADDDVLLSVL 386  
361 LVALPRWQNLHKGHRFADDDVLLSVL 386

RESULT 2  
ID AAB62653 standard; protein; 386 AA.  
AC AAB62653;  
XX 23-JUL-2001 (first entry)  
XX Short form of motilin receptor, GPR-38B isoform.  
XX zsig33; signal transduction; hormone; enzyme; neural development;  
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;  
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;  
KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38B; isoform.  
XX Homo sapiens.  
XX WO200138355-A2.  
XX 31-MAY-2001.  
XX 22-NOV-2000; 2000WO-US032074.  
XX 22-NOV-1999; 99US-0166765P.  
XX

(ZYMO ) ZYMOGENETICS INC.  
Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;  
WPI; 2001-355879/37.  
N-PSDB; AAF83684.  
Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide.  
Disclosure; Page 106-109; 111pp; English.  
The invention relates to a method of forming a reversible peptide-receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AAB62649), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and pancreatic enzymes and hormones, secretion of insulin-like growth factor -I, secretion of non-zsig33 proteins. It is useful for modulating growth hormone secretion in a mammal having a disease associated with abnormal levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the short form of motilin receptor, GPR-38B (one of the two isoforms of GPR38 which result from alternative splicing). GPR38 has homology to the human G-protein coupled receptor, GHS-R

Sequence 386 AA;  
Query Match 100.0%; Score 2043; DB 4; Length 386;  
Best Local Similarity 100.0%; Pred. No. 1e-171;  
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60  
1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60  
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120  
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120  
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180  
181 QDPGISVVPGLNCTARIASSPLASSPPLWLSRAPPSPGPGTAAALFRCRCPSPA 240  
181 QDPGISVVPGLNCTARIASSPLASSPPLWLSRAPPSPGPGTAAALFRCRCPSPA 240  
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300  
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300  
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360  
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360  
361 LVALPRWQNLHKGHRFADDDVLLSVL 386  
361 LVALPRWQNLHKGHRFADDDVLLSVL 386

RESULT 3

ADN11763  
 ID ADN11763 standard; protein; 386 AA.  
 AC ADN11763;  
 XX  
 XX  
 DT 15-JUL-2004 (first entry)  
 DE Human motilin receptor GPR-38B protein.  
 XX  
 XX human; zsig33; body weight; body mass; antibody; antagonist;  
 KW gastrointestinal; antiinflammatory; antitumor; vulnerary;  
 KW growth hormone secretagogue; GHS-R; peptide-antibody complex;  
 KW motilin receptor.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2004033645-A2.  
 PN  
 XX 22-APR-2004.  
 PD  
 XX 06-OCT-2003; 2003WO-US031804.  
 XX  
 PF 07-OCT-2002; 2002US-0416918P.  
 PP  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA  
 XX Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;  
 PI  
 XX WPI; 2004-340913/31.  
 DR N-PSDB; ADN11762.  
 DR  
 XX Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,  
 PT inhibiting signal transduction in a cell expressing a growth hormone  
 PT secretagogue receptor, or treating a metabolic disorder.  
 PT  
 XX Example 3; Page 98-99; 100pp; English.  
 PS  
 XX The present invention relates to the use of a zsig33 peptide for forming  
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal  
 CC transduction in a cell expressing a growth hormone secretagogue receptor  
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite  
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a  
 CC mammal, or treating a metabolic disorder. The peptide is useful for  
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting  
 CC signal transduction in a cell expressing a GHS-R, decreasing fat  
 CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting  
 CC growth hormone secretion in pituitary cells of a mammal, or treating a  
 CC metabolic disorder. The zsig33 polypeptides can be used to study  
 CC proliferation or differentiation in stomach, lung, pituitary,  
 CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,  
 CC skeletal muscle or pancreas. They are also useful in delivering  
 CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are  
 CC also useful for promoting wound healing. The polypeptides, nucleic acids  
 CC and antibodies are useful for diagnosing, treating or preventing  
 CC disorders associated with gastric reflux, gastroparesis, modulation of  
 CC secretion of pituitary hormones, including growth hormone, Crohn's  
 CC disease, metabolic wasting, gastric ulcers, weight management, or  
 CC degenerative disease. The present sequence is the human motilin receptor  
 CC GPR38B protein shown in the exemplification of the invention.  
 XX  
 XX Sequence 386 AA;  
 SQ  
 Query Match 100.0%; Score 2043; DB 8; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 1e-171;  
 Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGSPWNGSDGPGAREPPWALPPCDERRCSFPPLGALVPVTVAVCLCLFVVGVSNGVTV 60  
 DB |||||  
 1 MGSPWNGSDGPGAREPPWALPPCDERRCSFPPLGALVPVTVAVCLCLFVVGVSNGVTV 60  
 QY 61 MLIGYRDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSPWVFGPLCLRLSLYVGE 120  
 DB |||||  
 61 MLIGYRDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSPWVFGPLCLRLSLYVGE 120

121 CTYATLLHMTALSVERVLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGFFFLVGVE 180  
 121 CTYATLLHMTALSVERVLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGFFFLVGVE 180  
 181 QDPGISVVPGLNGTARTASSPLASSPPLWLSRAPPPSPSPETAANAALFSRECRPSPA 240  
 181 QDPGISVVPGLNGTARTASSPLASSPPLWLSRAPPPSPSPETAANAALFSRECRPSPA 240  
 241 QLGLARVWLWVTYAYFFLFCILSYGLIGRELWSSRRPLRGPAAASGRGRHGTVRVL 300  
 241 QLGLARVWLWVTYAYFFLFCILSYGLIGRELWSSRRPLRGPAAASGRGRHGTVRVL 300  
 301 RKWSRRGSKDACLOSAPPGTATGLPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360  
 301 RKWSRRGSKDACLOSAPPGTATGLPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360  
 361 LVALPRWQNHHLKHGRFADDDVLLSVL 386  
 361 LVALPRWQNHHLKHGRFADDDVLLSVL 386

RESULT 4  
 AAY54145  
 ID AAY54145 standard; protein; 412 AA.  
 AC AAY54145;  
 XX  
 XX 27-MAR-2000 (first entry)  
 DT  
 XX Amino acid sequence of the motilin receptor splice variant MTL-R1A.  
 DE  
 XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;  
 KW spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;  
 KW functional defect; neurological disorder; scleroderma; colonoscopy;  
 KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;  
 KW infection; stress-related motility disorder; psychogenic disorder;  
 KW gastroparesis; gastro-oesophageal reflux disease; constipation;  
 KW chronic idiopathic pseudo obstruction; acute faecal impaction;  
 KW postoperative ileus; gallstones; infantile colic; diarrhoea;  
 KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;  
 KW endoscopy; duodenal incubation.  
 XX  
 OS Homo sapiens.  
 XX WO9964436-A1.  
 PN  
 XX 16-DEC-1999.  
 PD  
 XX 08-JUN-1999; 99WO-US012773.  
 XX  
 XX 12-JUN-1998; 98US-0089098P.  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Feighner SD, Patchett AA, Tan C, Mckee K, Macneil D, Howard AD;  
 PI Pong S, Smith RG;  
 XX WPI; 2000-105868/09.  
 DR N-PSDB; AAY5403.  
 DR  
 XX Novel receptor protein for screening compounds used in treating irritable  
 PT bowel syndrome, constipation and other gastric conditions.  
 PT  
 XX Claim 3; Fig 3; 44pp; English.  
 PS  
 XX The present sequence represents splice variant MTL-R1A of the motilin  
 CC receptor. The gene encodes a G-protein coupled receptor, and is  
 CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A  
 CC (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven  
 CC transmembrane domain form, and MTL-R1B is a truncated five transmembrane  
 CC domain. The MTL-R1 proteins are used to identify agonists and antagonists  
 CC which can be used for treating gastric motility disorders, functional

CC defects, disorders secondary to neurological disorders e.g. scleroderma,  
 CC paraneoplastic syndromes radiation induced dysmotility, diabetes,  
 CC infections, stress-related motility disorders, psychogenic disorders,  
 CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic  
 CC idiopathic pseudo obstruction, acute faecal impaction, postoperative  
 CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer  
 CC dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used  
 CC in the preparation for colonoscopy, endoscopy and duodenal intubation  
 XX  
 SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 3; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-131;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPTAVTAVCLCLFVVGVSGNVTVV 60  
 DB 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPTAVTAVCLCLFVVGVSGNVTVV 60  
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120  
 DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLVLVGE 180  
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLVLVGE 180  
 QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPGTAAALFSRECRPSPA 240  
 DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPGTAAALFSRECRPSPA 240  
 QY 241 QLGLARVLMVLTWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300  
 DB 241 QLGLARVLMVLTWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300

RESULT 5  
 AAB68478  
 ID AAB68478 standard; protein; 412 AA.  
 XX  
 AC AAB68478;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human motilin receptor polypeptide.  
 XX  
 KW Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW gastroparesis; irritable bowel syndrome; diarrhoea.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132710-A1.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000WO-US029426.  
 XX  
 PR 29-OCT-1999; 99US-0162264P.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Tan C, McKee K;  
 XX  
 DR WPI; 2001-343479/36.  
 DR N-PSDB; AAF85449.  
 XX  
 PT Novel polypeptides related to dog and rabbit motilin receptor  
 PT polypeptide, comprising unique regions from dog and motilin receptor  
 PT amino acid sequence, useful for identifying compounds for treating  
 PT diarrhea in humans.  
 XX  
 PS Disclosure; Page 32-33; 42pp; English.  
 XX

CC The present sequence represents a human motilin receptor polypeptide. The  
 CC specification describes a unique sequence present in exon 1 of the dog  
 CC motilin receptor, which is not present in human or Sphaeroides nephelus  
 CC 7587 motilin receptor sequences. The unique nucleic acid sequence is  
 CC useful for measuring the ability of a compound to affect motilin receptor  
 CC activity. Motilin receptor polynucleotides and polypeptides are used to  
 CC identify therapeutic compounds which are useful for treating  
 CC gastrointestinal diseases and disorders such as gastric motility  
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea  
 XX  
 SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 4; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-131;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPTAVTAVCLCLFVVGVSGNVTVV 60  
 DB 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPTAVTAVCLCLFVVGVSGNVTVV 60  
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120  
 DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLVLVGE 180  
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLVLVGE 180  
 QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPGTAAALFSRECRPSPA 240  
 DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPGTAAALFSRECRPSPA 240  
 QY 241 QLGLARVLMVLTWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300  
 DB 241 QLGLARVLMVLTWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300

RESULT 6  
 AAB62652  
 ID AAB62652 standard; protein; 412 AA.  
 XX  
 AC AAB62652;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX  
 DE Long form of motilin receptor, GPR-38A isoform.  
 XX  
 KW zsig33; signal transduction; hormone; enzyme; neural development;  
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;  
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;  
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200138355-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 22-NOV-2000; 2000WO-US032074.  
 XX  
 PR 22-NOV-1999; 99US-0166765P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;  
 XX  
 DR WPI; 2001-355879/37.  
 DR N-PSDB; AAF83683.  
 XX  
 PT Forming reversible peptide receptor complex for purifying cell and  
 PT peptides, stimulating signal transduction and modulating hormone  
 PT secretion, involves contacting a receptor with zsig33 polypeptide.  
 XX

XX Disclosure; Page 102-104; illpp: English.

XX The invention relates to a method of forming a reversible peptide-receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AAB2649), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and pancreatic enzymes and hormones, secretion of insulin-like growth factor I, secretion of non-zsig33 proteins. It is useful for modulating growth hormone secretion in a mammal having a disease associated with abnormal levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the long form of motilin receptor, GPR-38A (one of the two isoforms of GPR38 which result from alternative splicing). GPR38 has homology to the human G-protein coupled receptor, GHS-R.

XX Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 4; Length 412;  
Best Local Similarity 100.0%; Pred. No. 6.6e-131;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60

QY 61 MLIGRYDMRTTNTLYLGSMAVSDLLILGLPFDLYRLWRSRPVFGPFLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNTLYLGSMAVSDLLILGLPFDLYRLWRSRPVFGPFLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVERVLAICRPLARVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERVLAICRPLARVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180

QY 181 QDQGISVVGNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRSPA 240  
Db 181 QDQGISVVGNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRSPA 240

QY 241 QLGALRVMLWVTYAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300  
Db 241 QLGALRVMLWVTYAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 7  
ABG30936  
ID ABG30936 standard; protein; 412 AA.  
AC ABG30936;  
XX  
XX 21-OCT-2002 (first entry)  
XX Human G protein-coupled receptor 38 (GPR38).  
XX Human; G protein-coupled receptor 38; receptor; GPR38;  
KW Alzheimer's disease; Parkinson's disease; ulcerative colitis;  
KW Crohn's disease; Hodgkin's disease; glioblastoma; breast carcinoma;  
KW colon carcinoma; lung small cell carcinoma; lung adenocarcinoma;  
KW pancreatic small cell carcinoma; pancreatic adenocarcinoma.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers

FT Region 15. .31  
FT /note= "Antigenic fragment"  
FT 217. .232  
FT /note= "Antigenic fragment"  
FT 276. .291  
FT /note= "Antigenic fragment"  
FT 373. .388  
FT /note= "Antigenic fragment"  
XX  
PN WO200257791-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 29-NOV-2001; 2001WO-US045219.  
XX  
XX 29-NOV-2000; 2000US-0250251P.  
XX  
XX 30-NOV-2000; 2000US-0250452P.  
XX  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
XX Brown JP, Burmer GC, Roush CL, Kulander BG;  
XX  
XX WPI; 2002-566812/60.  
XX  
XX N-FSDB; ABK90132.  
XX  
XX Assay for detecting Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma or carcinoma, comprises using a binding partner for G protein coupled receptor 38.  
XX  
XX Disclosure; Fig 2; 112pp; English.

XX The present invention relates to a new assay method that involves contacting a binding partner specific for G protein coupled receptor (GPR) 38 with specific cells. The method of the invention is useful for the detection of an increased risk of Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, or carcinoma. GPR 38 is used to manufacture a medicament for inhibiting, treating or preventing Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, breast carcinoma, colon carcinoma, lung small cell carcinoma, lung adenocarcinoma, pancreatic small cell carcinoma, and pancreatic adenocarcinoma. An agonist or antagonist to GPR 38 are used to manufacture a medicament able to reduce the symptoms of these diseases. Nucleic acids encoding GPR 38 can also be used to treat the diseases. The present amino acid sequence represents the human G protein-coupled receptor 38 (GPR38) of the invention

XX Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 5; Length 412;  
Best Local Similarity 100.0%; Pred. No. 6.6e-131;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
Db 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60

QY 61 MLIGRYDMRTTNTLYLGSMAVSDLLILGLPFDLYRLWRSRPVFGPFLCRLSLYVGE 120  
Db 61 MLIGRYDMRTTNTLYLGSMAVSDLLILGLPFDLYRLWRSRPVFGPFLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVERVLAICRPLARVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180  
Db 121 CTYATLLHMTALSVERVLAICRPLARVLTTRRRVRLIAVLWAVALLSAGPFLVGV 180

QY 181 QDQGISVVGNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRSPA 240  
Db 181 QDQGISVVGNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRSPA 240

QY 241 QLGALRVMLWVTYAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300  
Db 241 QLGALRVMLWVTYAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 8  
 ABP81993  
 ID ABP81993 standard; protein; 412 AA.  
 XX  
 AC ABP81993;  
 XX  
 04-MAR-2003 (first entry)  
 XX  
 DE Human motilin receptor GPR38 protein SEQ ID NO:473.  
 XX  
 DE G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261087-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050107.  
 XX  
 PR 19-DEC-2000; 2000US-0257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burner GC, Roush CL, Brown JP;  
 XX  
 DR WPI: 2003-046718/04.  
 DR N-PSDB; AB242842.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 FT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 533pp; English.  
 XX  
 CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention

## SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 6; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-131; Indels 0; Gaps 0;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGSPWNGSDGEGAREPPWALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGSGNVVTV 60  
 DB 1 MGSPWNGSDGEGAREPPWALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGSGNVVTV 60  
 QY 61 MLIGRYDMRTTNYLGSMVAVSDLLILGLPFLYRLWRSRPWVFGPFLCLSLYVGE 120  
 DB 61 MLIGRYDMRTTNYLGSMVAVSDLLILGLPFLYRLWRSRPWVFGPFLCLSLYVGE 120  
 QY 121 CTYATLHMTALSVERVLAICRPURARVLTTRRRVRLIAVLWAVALLSAGPFLFLVGVE 180  
 DB 121 CTYATLHMTALSVERVLAICRPURARVLTTRRRVRLIAVLWAVALLSAGPFLFLVGVE 180  
 QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSPA 240  
 DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSPA 240  
 QY 241 QLGALRVMLWVTYAYFPFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRVL 300  
 DB 241 QLGALRVMLWVTYAYFPFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRVL 300  
 RESULT 9  
 ADN11761  
 ID ADN11761 standard; protein; 412 AA.  
 XX  
 AC ADN11761;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human motilin receptor GPR-38A protein.  
 XX  
 KW human; zsig33; body weight; body mass; antibody; antagonist;  
 KW gastrointestinal; antiinflammatory; antiulcer; vulnerary;  
 KW growth hormone secretagogue; GHS-R; peptide-antibody complex;  
 KW motilin receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004033645-A2.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 06-OCT-2003; 2003WO-US031804.  
 XX  
 PR 07-OCT-2002; 2002US-0416918P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;  
 DR WPI: 2004-340913/31.  
 DR N-PSDB; ADN11760.  
 XX  
 PT Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,  
 FT inhibiting signal transduction in a cell expressing a growth hormone  
 PT secretagogue receptor, or treating a metabolic disorder.  
 XX  
 PS Disclosure; Page 95-96; 100pp; English.  
 XX  
 CC The present invention relates to the use of a zsig33 peptide for forming  
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal  
 CC transduction in a cell expressing a growth hormone secretagogue receptor  
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite  
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a  
 CC mammal, or treating a metabolic disorder. The peptide is useful for  
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting  
 CC signal transduction in a cell expressing a GHS-R, decreasing fat



CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting  
CC growth hormone secretion in pituitary cells of a mammal, or treating a  
CC metabolic disorder. The zsig33 polypeptides can be used to study  
CC proliferation or differentiation in stomach, lung, pituitary,  
CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,  
CC skeletal muscle or pancreas. They are also useful in delivering  
CC therapeutic agents. zsig33 polypeptides, agonists and antagonists are  
CC also useful for promoting wound healing. The polypeptides, nucleic acids  
CC and antibodies are useful for diagnosing, treating or preventing  
CC disorders associated with gastric reflux, gastroparesis, modulation of  
CC secretion of pituitary hormones, including growth hormone, Crohn's  
CC disease, metabolic wasting, gastric ulcers, weight management, or  
CC degenerative disease. The present sequence is the human motilin receptor  
CC GPR38A protein shown in the exemplification of the invention.  
XX  
SQ Sequence 412 AA;  
Query Match 77.4%; Score 1581; DB 8; Length 412;  
Best Local Similarity 100.0%; Pred. No. 6.6e-131;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVWVGSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVWVGSGNVTV 60  
QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVSG 120  
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVSG 120  
QY 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVALLIATLWALLSAGFFLVGVE 180  
Db 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVALLIATLWALLSAGFFLVGVE 180  
QY 181 QDPGIVSVPLNGTARIASSPLASSPPLWLSRAPPSPGSPETAEALFRCRCPSPA 240  
Db 181 QDPGIVSVPLNGTARIASSPLASSPPLWLSRAPPSPGSPETAEALFRCRCPSPA 240  
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASGRGHRQTVRL 300  
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASGRGHRQTVRL 300  
RESULT 10  
ADO29697  
ID ADO29697 standard; protein; 412 AA.  
XX  
AC ADO29697;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human GPCR GPR38, SEQ ID NO:799.  
XX  
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytostatic; antiinflammatory; vasotropic; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antiarthroic; antidiabetic;  
KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrheic;  
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
receptor.  
XX  
OS Homo sapiens.  
XX  
PN WO2004040000-A2.  
XX  
PD 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.  
PF  
XX 09-SEP-2003; 2002US-0409303P.  
XX  
PR 09-SEP-2003; 2003US-0461329P.  
XX  
XX (PRIM-) PRIMAL INC.  
PA  
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX  
XX WPI: 2004-390329/36.  
DR N-PSDB; ADO30072.  
XX  
PT Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
PS Claim 151; SEQ ID NO 799; 542pp; English.  
XX  
CC The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridize to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
CC invention. Note: The full sequence data for this patent did not form part  
CC of the printed specification; those sequences not shown were obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 412 AA;  
Query Match 77.4%; Score 1581; DB 8; Length 412;  
Best Local Similarity 100.0%; Pred. No. 6.6e-131;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVWVGSGNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCLCLFVWVGSGNVTV 60  
QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVSG 120  
Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVSG 120  
QY 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVALLIATLWALLSAGFFLVGVE 180  
Db 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVALLIATLWALLSAGFFLVGVE 180  
QY 181 QDPGIVSVPLNGTARIASSPLASSPPLWLSRAPPSPGSPETAEALFRCRCPSPA 240  
|||||

Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGSETAEAAALFSRECRPSPA 240  
 QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYLIGLRELSRRPLRGPAAASGRGRHRTVAVL 300  
 Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYLIGLRELSRRPLRGPAAASGRGRHRTVAVL 300

RESULT 11  
 ADQ37921  
 ID ADQ37921 standard; protein; 412 AA.  
 XX  
 AC ADQ37921;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human G-protein-coupled receptor 38 protein.  
 XX  
 KW antiparkinsonian; neuroprotective; nootropic; cardiovascular; cardiac;  
 KW vasotropic; antiarteriosclerotic; nephrotropic; uropathic;  
 KW urology disease; cardiovascular disease;  
 KW peripheral nervous system disorder; central nervous system disorder;  
 KW G-protein-coupled receptor 38; GPR38; Parkinson's disease;  
 KW multiple sclerosis; dementia; myocardial infarction; ischemic disease;  
 KW atherosclerosis; renal failure; glomerulopathy; urinary incontinence.  
 XX  
 OS Homo sapiens.  
 XX  
 PN .WO2004057328-A2.  
 XX  
 PD 08-JUL-2004.  
 XX  
 PF 11-DEC-2003; 2003WO-EP014052.  
 XX  
 PR 23-DEC-2002; 2002EP-00028753.  
 XX  
 PA (FARB ) BAYER HEALTHCARE AG.  
 XX  
 PI Golz S, Brueggemeier U, Summer H;  
 XX  
 DR WPI: 2004-543310/52.  
 DR N-PSDB; ADQ37920.  
 XX  
 PT Screening therapeutic agents for use in treatment of urology diseases and  
 PT cardiovascular diseases in a mammal, comprises contacting a test compound  
 PT with G-protein-coupled receptor 38, and detecting binding.  
 XX  
 PS Disclosure; SEQ ID NO 2; 11pp; English.  
 CC  
 CC The invention relates to a method of screening (M1) for therapeutic  
 CC agents useful in the treatment of a disease chosen from urology diseases,  
 CC cardiovascular diseases and disorders of the peripheral and central  
 CC nervous system in a mammal, comprises contacting a test compound with a G  
 CC -protein-coupled receptor 38 (GPR38) polypeptide, and detecting binding  
 CC of the test compound to the GPR38 polypeptide. (M1) is useful for  
 CC screening therapeutic agents useful in the treatment of a disease chosen  
 CC from urology diseases, cardiovascular diseases and disorders of the  
 CC peripheral and central nervous system in a mammal, such as Parkinson's  
 CC disease, multiple sclerosis, dementia, cardiovascular disorders such as  
 CC myocardial infarction, ischemic diseases, atherosclerosis, and urological  
 CC disorders such as acute or chronic renal failure, glomerulopathies, and  
 CC urinary incontinence. This sequence corresponds to the human G-protein-  
 CC coupled receptor 38.  
 XX  
 SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 8; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-131;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDPGAGREPPPALPCDRECSFPFLGALVPVTAICLFLVGVGNGVNTV 60  
 Db 1 MGSPWNGSDPGAGREPPPALPCDRECSFPFLGALVPVTAICLFLVGVGNGVNTV 60

QY 61 MLIGRYDMRTTTLNLYLGSMVAVDLLILLGLPFDLYRLWRSRPVWFGPLLCRLSLYVGE 120  
 Db 61 MLIGRYDMRTTTLNLYLGSMVAVDLLILLGLPFDLYRLWRSRPVWFGPLLCRLSLYVGE 120  
 QY 121 CTYATLLHMTALSVERVLAICRPLRARVLTTRRVRAIAVLWAVALLSAGPFLVGVGE 180  
 Db 121 CTYATLLHMTALSVERVLAICRPLRARVLTTRRVRAIAVLWAVALLSAGPFLVGVGE 180  
 QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGSETAEAAALFSRECRPSPA 240  
 Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGSETAEAAALFSRECRPSPA 240  
 QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYLIGLRELSRRPLRGPAAASGRGRHRTVAVL 300  
 Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYLIGLRELSRRPLRGPAAASGRGRHRTVAVL 300

RESULT 12  
 AAG65822  
 ID AAG65822 standard; protein; 501 AA.  
 XX  
 AC AAG65822;  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE Human GPR38 variant GPR38V polypeptide.  
 XX  
 DE  
 KW GPR38V; variant; antibacterial; cytostatic; analgesic; antiasthmatic;  
 KW anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic;  
 KW anti-allergic; antimigraine; neuroleptic; nootropic; anticonvulsant;  
 KW anti-ulcer; antiemetic; cardiac; vaccine; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000164836-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US006277.  
 XX  
 PR 01-MAR-2000; 2000US-00516315.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Elshourbagy N, Shabon U;  
 XX  
 DR WPI: 2001-638956/73.  
 DR N-PSDB; AAI65989.  
 XX  
 PT New human GPR38V polypeptide and polynucleotide, useful for treating e.g.  
 PT bacterial, fungal, protozoal and viral infections, cancers or allergies,  
 PT as vaccines, and for identifying agonists and antagonists potentially  
 PT useful in therapy.  
 XX  
 PS Claim 1; Page 26; 32pp; English.  
 XX  
 CC This represents a human GPR38 variant (GPR38V) polypeptide. GPR38V can be  
 CC expressed by standard recombinant methodology. The polynucleotides and  
 CC polypeptides are used in the treatment of bacterial, fungal, protozoal  
 CC and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,  
 CC diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart  
 CC failure, hypertension, urinary retentions, osteoporosis, allergies,  
 CC ulcers, migraine, psychotic and neurological disorders, or dyskinesias.  
 CC They are also useful for identifying agonists and antagonists that are  
 CC potentially useful in therapy, as vaccines to induce immunological  
 CC response in a mammal. The polypeptides may also be used as immunogens to  
 CC produce antibodies immunospecific for the polypeptides, and to identify  
 CC membrane bound or soluble receptors  
 XX  
 SQ Sequence 501 AA;

Query Match 77.4%; Score 1581; DB 4; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-131;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 60

Db 90 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 149

Qy 61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 120

Db 150 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 209

Qy 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180

Db 210 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 269

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

Db 270 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 329

Qy 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHRTVRVL 300

Db 330 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHRTVRVL 389

RESULT 13

AAB02854

ID AAB02854 standard; protein; 412 AA.

XX AC AAB02854;

DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hGPR38 (V297K) protein SEQ ID NO:130.

XX DE Human; G protein coupled receptor; GPCR; transmembrane receptor;

KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US024065.

XX PR 13-OCT-1998; 98US-00170496.

PR 12-NOV-1998; 98US-0108029P.

PR 20-NOV-1998; 98US-0109213P.

PR 27-NOV-1998; 98US-0110060P.

PR 16-FEB-1999; 99US-0120416P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123944P.

PR 12-MAR-1999; 99US-0123945P.

PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123948P.

PR 12-MAR-1999; 99US-0123949P.

PR 28-MAY-1999; 99US-0123951P.

PR 28-MAY-1999; 99US-0136436P.

PR 28-MAY-1999; 99US-0136437P.

PR 28-MAY-1999; 99US-0136439P.

PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.

PR 28-MAY-1999; 99US-0137567P.

PR 29-JUN-1999; 99US-0141448P.

PR 27-AUG-1999; 99US-0151114P.

PR 03-SEP-1999; 99US-0152524P.

PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.

PR 29-SEP-1999; 99US-0156634P.

PR 29-SEP-1999; 99US-0156653P.

PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.

PR 01-OCT-1999; 99US-0157293P.

PR 01-OCT-1999; 99US-0157294P.

PR 12-OCT-1999; 99US-00416760.

PR 12-OCT-1999; 99US-00417044.

XX (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

XX N-PSDB; AAA46116.

DR WPI; 2000-317986/27.

XX DR N-PSDB; AAA46116.

XX Non-endogenous, human G protein-coupled receptors for screening receptor,

PT inverse or partial agonists useful as therapeutic agents.

XX Example 2; Page 168-169; 187pp; English.

XX The present invention describes transmembrane receptors, preferably human

CC G protein coupled receptors (GPCR), for which the endogenous ligand is

CC unknown (orphan GPCR receptors). More specifically the present invention

CC relates to non-endogenous, constitutively activated versions of a human

CC GPCR. These non-endogenous human GPCRs can be useful for the direct

CC identification of candidate compounds as receptors agonists, inverse

CC agonists or partial agonists for use as pharmaceutical agents. AAA46017

CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the

CC exemplification of the present invention

XX Sequence 412 AA;

Qy Query Match 77.1%; Score 1575; DB 3; Length 412;

Best Local Similarity 99.7%; Pred. No. 2.2e-130;

Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 60

Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCLCLFVVGSGNVTV 60

Qy 61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 120

Db 61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 120

Qy 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180

Db 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

Qy 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHRTVRVL 300

Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHRTVRVL 300

RESULT 14

ADG86491

ID ADG86491 standard; protein; 412 AA.

XX AC ADG86491;

XX 11-MAR-2004 (first entry)

XX Human hGPR38 V297K mutant protein.

XX Human; receptor; mutein; endogenous orphan GPCR;

KW G protein-coupled receptor; transmembrane domain 6; mutant.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US2003229216-A1.

XX PN

PD 11-DEC-2003.  
 XX 16-APR-2003; 2003US-00417820.  
 PF 13-OCT-1998; 98US-00170496.  
 XX 12-NOV-1998; 98US-0108029P.  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 27-NOV-1998; 98US-0110060P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123944P.  
 PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123951P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 27-AUG-1999; 99US-0151114P.  
 PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 XX (CHEN/) CHEN R.  
 PA (LIAN/) LIAN C W.  
 PA (LOWI/) LOWITZ K.  
 PA (CHAL/) CHALMERS D T.  
 PA (BEHA/) BEHAN D P.  
 XX Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;  
 PI WPI; 2004-052038/05.  
 DR N-PSDB; ADG86490.  
 XX New cDNA encoding a non-endogenous, constitutively activated version of a  
 PT human G protein-coupled receptor, useful for identifying receptor,  
 PT inverse or partial agonists having potential applicability as therapeutic  
 PT agents.  
 XX Example 2; SEQ ID NO 130; 110pp; English.  
 PS The invention relates to a cDNA encoding a non-endogenous, constitutively  
 XX activated version of a human G protein-coupled receptor comprising HARE-  
 CC 3 (F313K), HARE-4 (V233K), HARE-5 (A240K), hGPCR14 (L257K), hGPCR27 (C283K),  
 CC HARE-1 (E232K), HARE-2 (G285K), hPR1 (L239K), hG2A (K232A), hRUP3 (L224K),  
 CC hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K),  
 CC hCHN3 (S284K), hCHN6 (L355K), hCHN8 (N235K) or hH9 (F236K). Also included are  
 CC a non-endogenous version of a human G protein-coupled receptor encoded by  
 CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell  
 CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively  
 CC activated version of a human G protein-coupled AT1 receptor comprising  
 CC the angiotensin II type 1 receptor hAT1 (F239K), hAT1 (N11A),  
 CC hAT1 (AT2K255IC3), a domain swap mutant or hAT1 (A243+). The mutation is of  
 CC an amino acid 16 residues from the proline in transmembrane domain 6 and  
 CC is usually to a lysine. The cDNA is useful for identifying candidate  
 CC compounds as receptor agonists, inverse agonists or partial agonists  
 CC having potential applicability as therapeutic agents. The present  
 CC sequence represents a mutated human GPCR.  
 XX Sequence 412 AA;

Query Match 77.1%; Score 1575; DB 8; Length 412;  
 Best Local Similarity 99.7%; Pred. No. 2.2e-130; Mismatches 1; Indels 0; Gaps 0;  
 Matches 299; Conservative 0;  
 QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPFPGALVPVTAVCLCLFVVGVSNGVTV 60  
 DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPFPGALVPVTAVCLCLFVVGVSNGVTV 60  
 QY 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
 DB 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
 QY 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
 DB 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180  
 QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPPPETAEEAALFSRECRPSPA 240  
 DB 181 QDPGISVVPGLNGTARIASSPPLASSPPLWLSRAPPPSPPPETAEEAALFSRECRPSPA 240  
 QY 241 QLGALRVMLVTTTAYFFLPFLCLSLYGLIORELMSSRRPLRGPAASGRERGHRTVRL 300  
 DB 241 QLGALRVMLVTTTAYFFLPFLCLSLYGLIORELMSSRRPLRGPAASGRERGHRTVRL 300  
 RESULT 15  
 ADG86511  
 ID ADG86511 standard; protein; 412 AA.  
 XX AC ADG86511;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Human orphan GPCR-associated protein #2.  
 XX KW Human; endogenous orphan GPCR; G protein-coupled receptor;  
 KW transmembrane domain 6.  
 XX OS Homo sapiens.  
 XX PN US2003229216-A1.  
 XX PD 11-DEC-2003.  
 XX PF 16-APR-2003; 2003US-00417820.  
 XX PR 13-OCT-1998; 98US-00170496.  
 PR 12-NOV-1998; 98US-0108029P.  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 27-NOV-1998; 98US-0110060P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123944P.  
 PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 12-MAR-1999; 99US-0123951P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 27-AUG-1999; 99US-0151114P.  
 PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.  
PR 01-OCT-1999; 99US-0157282P.  
PR 01-OCT-1999; 99US-0157293P.  
PR 01-OCT-1999; 99US-0157294P.  
PR 12-OCT-1999; 99US-00416760.  
XX  
PA (CHEN/) CHEN R.  
PA (LIAN/) LIAN C W.  
PA (LOWI/) LOWITZ K.  
PA (CHAL/) CHALMERS D T.  
PA (BEHA/) BEHAN D P.  
XX  
PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;  
XX  
DR WPI; 2004-052038/05.  
XX  
XX New cDNA encoding a non-endogenous, constitutively activated version of a  
PT human G protein-coupled receptor, useful for identifying receptor,  
PT inverse or partial agonists having potential applicability as therapeutic  
PT agents.  
XX  
PS Disclosure; SEQ ID NO 150; 110pp; English.  
XX  
CC The invention relates to a cDNA encoding a non-endogenous, constitutively  
CC activated version of a human G protein-coupled receptor comprising HARE-  
CC 3(F313K), HARE-4(V233K), HARE-5(A240K), hGPCR14(L257K), hGPCR27(C283K),  
CC HARE-1(E232K), HARE-2(G285K), hPR1 (L239K), hG2A(K232A), hRUP3(L224K),  
CC hRUP5(A236K), hRUP6(N267K), hRUP7(A302K), hCHN4(V236K), hMC4(V244K),  
CC hCHN3(S284K), hCHN6(L352K), hCHN8(N235K), or hH9(F236K). Also included are  
CC a non-endogenous version of a human G protein-coupled receptor encoded by  
CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell  
CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively  
CC activated version of a human G protein-coupled AT1 receptor comprising  
CC the angiotensin II type 1 receptor hAT1(F239K), hAT1(N111A),  
CC hAT1(A22K355IC3, a domain swap mutant) or hAT1(A243+). The mutation is of  
CC an amino acid 16 residues from the proline in transmembrane domain 6 and  
CC is usually to a lysine. The cDNA is useful for identifying candidate  
CC compounds as receptor agonists, inverse agonists or partial agonists  
CC having potential applicability as therapeutic agents. The present  
CC sequence is a GPCR-associated protein included in the sequence listing  
CC but not mentioned anywhere else in the specification.  
XX  
SQ Sequence 412 AA;  
Query Match 77.1%; Score 1575; DB 8; Length 412;  
Best Local Similarity 99.7%; Pred. No. 2.2e-130;  
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPFPLGALVPVTA VCLCLFVVGSGNVTV 60  
Db |||||  
1 MGSPWNGSDGPGAREPPWALPPCDERRCSPFPLGALVPVTA VCLCLFVVGSGNVTV 60  
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLIILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
Db |||||  
61 MLIGRYDRMTTNNLYLGSMAVSDLLIILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
QY 121 CTYATLLHMTALSVRYLAICRLRLARVLVTRRRYALIAVLMAVALLSAGPFLVLGVE 180  
Db |||||  
121 CTYATLLHMTALSVRYLAICRLRLARVLVTRRRYALIAVLMAVALLSAGPFLVLGVE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPETAEEAALFSRECRSPA 240  
Db |||||  
181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPETAEEAALFSRECRSPA 240  
QY 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHROTIVL 300  
Db |||||  
241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHROTIVL 300

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Job time : 65.3333 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 11, 2005, 20:05:13 ; Search time 19.8321 Seconds  
(without alignments)  
1452.926 Million cell updates/sec

Title: US-09-719-485-5  
Perfect score: 2043  
Sequence: 1 MGSPWNGSDGEGAREPWP.....WQNLHKRGFPADVLLSVL 386

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1581	77.4	412	US-09-743-742B-8	Sequence 8, Appli
2	649	31.8	289	US-09-077-675A-10	Sequence 10, Appl
3	649	31.8	289	US-09-077-674-10	Sequence 10, Appl
4	644	31.5	349	US-09-762-661A-2	Sequence 2, Appli
5	643	31.5	366	US-09-077-675A-13	Sequence 13, Appl
6	643	31.5	366	US-09-077-674-13	Sequence 13, Appl
7	643	31.5	366	US-09-170-496D-88	Sequence 88, Appl
8	643	31.5	366	US-09-743-742B-7	Sequence 7, Appli
9	643	31.5	366	US-09-762-661A-5	Sequence 5, Appli
10	643	31.5	366	US-09-364-425B-45	Sequence 45, Appl
11	643	31.5	366	US-09-743-475-4	Sequence 4, Appli
12	641	31.4	289	US-09-077-675A-5	Sequence 5, Appli
13	641	31.4	289	US-09-077-674-5	Sequence 5, Appli
14	641	31.4	364	US-09-077-675A-16	Sequence 16, Appl
15	641	31.4	364	US-09-077-674-16	Sequence 16, Appl
16	641	31.4	364	US-09-762-661A-6	Sequence 6, Appli
17	641	31.4	364	US-09-743-475-3	Sequence 3, Appli
18	641	31.4	364	US-09-743-475-5	Sequence 5, Appli
19	641	31.4	366	US-09-762-661A-7	Sequence 7, Appli
20	641	31.4	366	US-09-743-475-6	Sequence 6, Appli
21	639.5	31.3	353	US-09-077-675A-3	Sequence 3, Appli
22	639.5	31.3	353	US-09-077-674-3	Sequence 3, Appli
23	639.5	31.3	361	US-09-077-675A-8	Sequence 8, Appli
24	639.5	31.3	361	US-09-077-674-8	Sequence 8, Appli
25	637	31.2	366	US-09-170-496D-210	Sequence 210, App
26	554	27.1	302	US-09-077-675A-7	Sequence 7, Appli
27	554	27.1	302	US-09-077-674-7	Sequence 7, Appli

28	552	27.0	302	3	US-09-077-675A-2	Sequence 2, Appli
29	552	27.0	302	4	US-09-077-674-2	Sequence 2, Appli
30	454	22.2	271	3	US-09-077-675A-12	Sequence 12, Appl
31	454	22.2	271	4	US-09-077-674-12	Sequence 12, Appl
32	354.5	17.4	403	4	US-09-170-496D-114	Sequence 114, App
33	354.5	17.4	403	4	US-09-743-742B-4	Sequence 4, Appli
34	354.5	17.4	403	4	US-09-743-742B-10	Sequence 10, Appl
35	352.5	17.3	403	4	US-09-170-496D-224	Sequence 224, App
36	335	16.4	412	4	US-09-949-016-10101	Sequence 10101, A
37	335	16.4	415	4	US-09-545-944-2	Sequence 2, Appli
38	335	16.4	415	4	US-09-341-016A-1	Sequence 1, Appli
39	333	16.3	242	4	US-09-694-725-2	Sequence 2, Appli
40	331.5	16.2	405	4	US-09-743-742B-2	Sequence 2, Appli
41	331.5	16.2	405	4	US-09-743-742B-11	Sequence 11, Appli
42	330	16.2	418	4	US-09-743-742B-5	Sequence 5, Appli
43	326.5	16.0	418	4	US-09-826-509-535	Sequence 535, App
44	322	15.8	353	1	US-08-118-270-45	Sequence 45, Appl
45	322	15.8	353	5	PCT-US93-08528-45	Sequence 45, Appl

## ALIGNMENTS

RESULT 1  
US-09-743-742B-8  
; Sequence 8, Application US/09743742B  
; Patent No. 6599718  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Qingyun  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: McKee, Karen Kufju  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED  
; TITLE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS  
; FILE REFERENCE: 20217YP  
; CURRENT APPLICATION NUMBER: US/09/743,742B  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: PCT/US99/15941  
; PRIOR FILING DATE: 1999-07-13  
; PRIOR APPLICATION NUMBER: 60/092,623  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-743-742B-8

Query Match	77.4%	Score 1581;	DB 4;	Length 412;
Best Local Similarity	100.0%;	Pred. No. 3.7e-123;		
Matches 300;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGSPWNGSDGEGAREPWPALPCDERRCSPFPGLGALVPVTAVCLCLFVVGSGNVTV	60	
Db	1	MGSPWNGSDGEGAREPWPALPCDERRCSPFPGLGALVPVTAVCLCLFVVGSGNVTV	60	
Qy	61	MLIGRYDMRTTNYLGSMASVSDLLILGHPDLYRLWRSPWVFGPGLLCRLSLYVGEG	120	
Db	61	MLIGRYDMRTTNYLGSMASVSDLLILGHPDLYRLWRSPWVFGPGLLCRLSLYVGEG	120	
Qy	121	CTYATLHMTALSVERVLAICRPLRVRVLTTRRRVRLIAVLWAVALLSAGPFLVGVE	180	
Db	121	CTYATLHMTALSVERVLAICRPLRVRVLTTRRRVRLIAVLWAVALLSAGPFLVGVE	180	
Qy	181	QDPGISVVGGLNGTARTASSPPLWLSRAPPPSPSPETAAALFSRECRPSPA	240	
Db	181	QDPGISVVGGLNGTARTASSPPLWLSRAPPPSPSPETAAALFSRECRPSPA	240	
Qy	241	QLGALRVMLWTTTAYFFLPFLCLSLTYGLIGRELWSSRPLRGPAASGRGHRTQTVRL	300	
Db	241	QLGALRVMLWTTTAYFFLPFLCLSLTYGLIGRELWSSRPLRGPAASGRGHRTQTVRL	300	

## RESULT 2

US-09-077-675A-10  
; Sequence 10, Application US/09077675A  
; Patent No. 6242199  
; GENERAL INFORMATION:  
; APPLICANT: Pai, Lee-Yuh  
; APPLICANT: Feighner, Scott C.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Pong, Sheng-Shung  
; APPLICANT: Van Der Ploeg, Leonardus H.T.  
; TITLE OF INVENTION: RECEPTOR ASSAY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,675A  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19590P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 289 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-077-675A-10

Query Match 31.8%; Score 649; DB 3; Length 289;  
Best Local Similarity 43.2%; Pred. No. 4.3e-46;  
Matches 145; Conservative 46; Mismatches 87; Indels 58; Gaps 8;  
QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPPLGALVPVTAIVCLCLFVVGVSGN 56  
DB 2 WNATPEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGVIAGN 61  
QY 57 VVTVMILGRYDRMTTNNLYGSMVAVSDLLILLGLPEDLYRLWRSRPMVFGPLLCRLSLY 116  
DB 62 LUTMLVRSFRRLTNNLYGSMVAVSDLLIFLCMPDLVLRLWQYRPNWFGDLCKLFQF 121  
QY 117 VGEGETYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLALIVLWAVALLSAGPFLFL 176  
DB 122 VSESCTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181  
QY 177 VGVQDPGIVVVGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRRCR 236  
DB 182 VGVHE-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQLGALRVLWVTTTAYVFFPLCLISLYGLIGRELWSSRRPLRGPAASGRGHR 294  
DB 200 PTEFAVRSGLLVWVWSIFFPLVFCVTUYSILIGRLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTVRLRKWSRSGKDACIQSAPPGTAQTGLPLPL 330

Db 260 QTVKML-----GGSQRALRLSLAGPIILSLCLPLSL 289

## RESULT 3

US-09-077-674-10  
; Sequence 10, Application US/09077674  
; Patent No. 6531314  
; GENERAL INFORMATION:  
; APPLICANT: Arena, Joseph P.  
; APPLICANT: Cully, Doris F.  
; APPLICANT: Feighner, Scott D.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Liberator, Paul A.  
; APPLICANT: Schaeffer, James M.  
; APPLICANT: Van Der Ploeg, Leonardus  
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/077,674  
; FILING DATE: 3-JUN-1998  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cocuzzo, Anna L.  
; REGISTRATION NUMBER: 42,452  
; REFERENCE/DOCKET NUMBER: 19589P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-1273  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 289 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-077-674-10

Query Match 31.8%; Score 649; DB 4; Length 289;  
Best Local Similarity 43.2%; Pred. No. 4.3e-46;  
Matches 145; Conservative 46; Mismatches 87; Indels 58; Gaps 8;  
QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPPLGALVPVTAIVCLCLFVVGVSGN 56  
DB 2 WNATPEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGVIAGN 61  
QY 57 VVTVMILGRYDRMTTNNLYGSMVAVSDLLILLGLPEDLYRLWRSRPMVFGPLLCRLSLY 116  
DB 62 LUTMLVRSFRRLTNNLYGSMVAVSDLLIFLCMPDLVLRLWQYRPNWFGDLCKLFQF 121  
QY 117 VGEGETYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLALIVLWAVALLSAGPFLFL 176  
DB 122 VSESCTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181  
QY 177 VGVQDPGIVVVGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRRCR 236  
DB 182 VGVHE-----NGT-----DP--W-----DTNECR 199





APPLICANT: Howard, Andrew D.  
APPLICANT: Liberator, Paul A.  
APPLICANT: Schaeffer, James M.  
APPLICANT: Van Der Ploeg, Leonardus  
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Metck & Co., Inc.  
STREET: P.O. Box 2000, 126 B. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/077,674  
FILING DATE: 3-JUN-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cocuzzo, Anna L.  
REGISTRATION NUMBER: 42,452  
REFERENCE/DOCKET NUMBER: 19589P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1273  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-077-674-13

Query Match 31.5%; Score 643; DB 4; Length 366;  
Best Local Similarity 45.1%; Pred. No. 1.8e-45;  
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;  
QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPPFLGALVPTAVCLCLFVVGVSGN 56  
DB 2 WNATPSEPGFNLTADLDWDASPGNDSLGDELLQFPAPLLAGVTATCTVALFVVVGIA 61  
QY 57 VVTVMILGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGPLLCRLSLY 116  
DB 62 LLTMLVSRFRRLRTTNLYLSSMAFSDLLIFLCPLDLVRLWQYRPNWFGDLCKLQF 121  
QY 117 VGEGETYATLLHMTALSVERYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176  
DB 122 VSECTYATLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFVL 181  
QY 177 VGVQDPGISVVGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRRCR 236  
DB 182 VGVEHE-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQLGALVRLWVTTAYFFLPFLCLSLYLGILGRELWSSRRPLRGPAAASGRGHR 294  
DB 200 PTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTVRVL 300  
DB 260 QTVKML 265

RESULT 7

US-09-170-496D-88

Sequence 88, Application US/09170496D  
Patent No. 6555339  
GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G Protein-  
FILE REFERENCE: ASEN-0040  
CURRENT APPLICATION NUMBER: US/09/170,496D  
CURRENT FILING DATE: 1998-10-13  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 88  
LENGTH: 366  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-170-496D-88

Query Match 31.5%; Score 643; DB 4; Length 366;  
Best Local Similarity 45.1%; Pred. No. 1.8e-45;  
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;  
QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPPFLGALVPTAVCLCLFVVGVSGN 56  
DB 2 WNATPSEPGFNLTADLDWDASPGNDSLGDELLQFPAPLLAGVTATCTVALFVVVGIA 61  
QY 57 VVTVMILGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGPLLCRLSLY 116  
DB 62 LLTMLVSRFRRLRTTNLYLSSMAFSDLLIFLCPLDLVRLWQYRPNWFGDLCKLQF 121  
QY 117 VGEGETYATLLHMTALSVERYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176  
DB 122 VSECTYATLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFVL 181  
QY 177 VGVQDPGISVVGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRRCR 236  
DB 182 VGVEHE-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQLGALVRLWVTTAYFFLPFLCLSLYLGILGRELWSSRRPLRGPAAASGRGHR 294  
DB 200 PTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTVRVL 300  
DB 260 QTVKML 265

RESULT 8

US-09-743-742B-7

Sequence 7, Application US/09743742B  
Patent No. 6599718  
GENERAL INFORMATION:  
APPLICANT: Liu, Qingyun  
APPLICANT: Howard, Andrew D.  
APPLICANT: McKee, Karen Kujju  
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED  
FILE REFERENCE: 20217YP  
CURRENT APPLICATION NUMBER: US/09/743,742B  
CURRENT FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: PCT/US99/15941  
PRIOR FILING DATE: 1999-07-13  
PRIOR APPLICATION NUMBER: 60/092,623  
PRIOR FILING DATE: 1998-07-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 366  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-743-742B-7

Query Match 31.5%; Score 643; DB 4; Length 366;  
Best Local Similarity 45.1%; Pred. No. 1.8e-45;  
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVGVSGN 56  
DB 2 WNATPSEEPGFNLTLADLDWDASPGNDSLGLDELQLFPAPLAGVTATCVALLFVVGIAGN 61  
QY 57 VVTVMILIGRYDRMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWVFGPGLCLSLY 116  
DB 62 LLTMLVVSFRFRELRTTNLYLSSMAFSDLLIFLCPLDLVRLWQYRPNWFGDLCKLQFQ 121  
QY 117 VGEQCTYATLLHMTALSVERYLAICRPLARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176  
DB 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181  
QY 177 VGEQDPGIVSVVPGVGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236  
DB 182 VGVHE-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQIGALRVMLVWTTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHR 294  
DB 200 PTEFAVRSGLLTVMVWSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTVRVL 300  
DB 260 QTVKML 265

## RESULT 9

US-09-762-661A-5  
; Sequence 5, Application US/09762661A  
; Patent No. 6645726  
; GENERAL INFORMATION:  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Palyana, Oksana C.  
; APPLICANT: Smith, Roy G.  
; APPLICANT: Tan, Carina P.  
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE  
; FILE REFERENCE: 20207P  
; CURRENT APPLICATION NUMBER: US/09/762,661A  
; CURRENT FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/17915  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/095,960  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-762-661A-5

Query Match 31.5%; Score 643; DB 4; Length 366;  
Best Local Similarity 45.1%; Pred. No. 1.8e-45;  
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVGVSGN 56  
DB 2 WNATPSEEPGFNLTLADLDWDASPGNDSLGLDELQLFPAPLAGVTATCVALLFVVGIAGN 61  
QY 57 VVTVMILIGRYDRMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWVFGPGLCLSLY 116  
DB 62 LLTMLVVSFRFRELRTTNLYLSSMAFSDLLIFLCPLDLVRLWQYRPNWFGDLCKLQFQ 121  
QY 117 VGEQCTYATLLHMTALSVERYLAICRPLARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176  
DB 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181  
QY 177 VGEQDPGIVSVVPGVGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236  
DB 182 VGVHE-----NGT-----DP--W-----DTNECR 199

Db 182 VGVHE-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQIGALRVMLVWTTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHR 294  
Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTVRVL 300  
Db 260 QTVKML 265

## RESULT 10

US-09-364-425B-45  
; Sequence 45, Application US/09364425B  
; Patent No. 6653086  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Chen, Ruoping  
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor  
; FILE REFERENCE: Aten0047  
; CURRENT APPLICATION NUMBER: US/09/364,425B  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/094,879  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: 60/106,300  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 60/110,906  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 45  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-364-425B-45

Query Match 31.5%; Score 643; DB 4; Length 366;  
Best Local Similarity 45.1%; Pred. No. 1.8e-45;  
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY 5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTA VCLCLFVVGVSGN 56  
DB 2 WNATPSEEPGFNLTLADLDWDASPGNDSLGLDELQLFPAPLAGVTATCVALLFVVGIAGN 61  
QY 57 VVTVMILIGRYDRMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWVFGPGLCLSLY 116  
DB 62 LLTMLVVSFRFRELRTTNLYLSSMAFSDLLIFLCPLDLVRLWQYRPNWFGDLCKLQFQ 121  
QY 117 VGEQCTYATLLHMTALSVERYLAICRPLARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176  
DB 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181  
QY 177 VGEQDPGIVSVVPGVGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236  
DB 182 VGVHE-----NGT-----DP--W-----DTNECR 199  
QY 237 PS--PAQIGALRVMLVWTTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHR 294  
DB 200 PTEFAVRSGLLTVMVWSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259  
QY 295 QTVRVL 300  
DB 260 QTVKML 265

## RESULT 11

US-09-743-475-4



; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065-0900  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/077,674  
 ; FILING DATE: 3-JUN-1998  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cocuzzo, Anna L.  
 ; REGISTRATION NUMBER: 42,452  
 ; REFERENCE/DOCKET NUMBER: 19589P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 732-594-1273  
 ; TELEFAX: 732-594-4720  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 289 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-077-674-5

Query Match 31.4%; Score 641; DB 4; Length 289;

Best Local Similarity 43.3%; Pred. No. 2e-45;  
Matches 142; Conservative 45; Mismatches 77; Indels 64; Gaps 9;

QY 5 WNGSDGPGA-----REPWPALPCD---ERRCSPPFLGALVPTAVCLCLFVVGSGN 56  
 DB 2 WNATSEBPGNLTLPDGLGWDAPPENDSLVEELLPLFTPLLAGVTATCVLFFVVGAGN 61  
 QY 57 VVTMLIGRYDMRTTNTNLYLGSMAVSDLLILGLPFDLYLRWRSRPWVFGPLLCRLSLY 116  
 DB 62 LLTMLVSRPREMTTNTNLYLSSMAFSELLFLCMLPELFLMQYRPNNLGNLCKLQF 121  
 QY 117 VGECTYATLLHMTALSVERYLAICRPLRARVLTTRRVRALIAVLAVALLSAGPFLFL 176  
 DB 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVILVIWAVAFCSAGPIFVL 181  
 QY 177 VGVEODPGISVVGNGTARTASSPLASSPPLMLSRAPPSPPGPETAEEAALFSRECR 236  
 DB 182 VGVEHD-----NGT-----DPRD-----TNECR 199  
 QY 237 PS--PAQGLARVLMVWTTAYFFLPFLCLSIYLGILGRELMSRRPLRGPAASG---RER 291  
 DB 200 ATEPAVRSGLLTVMVWVSSVFFFLVFCLTVLYSLIGRKLW---RRKGEAAVGSLLRDQ 256  
 QY 292 GHRQTVRLKWSRRGSKDACLSAPPG 319  
 DB 257 NHHQTVKML-----GGSQCALELSLP 278

## RESULT 14

US-09-077-675A-16  
 ; Sequence 16, Application US/09077675A  
 ; Patent No. 6242199  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pai, Lee-Yuh  
 ; APPLICANT: Feighner, Scott C.  
 ; APPLICANT: Howard, Andrew D.

; APPLICANT: Pong, Sheng-Shung  
 ; APPLICANT: Van Der Ploeg, Leonardus H.T.  
 ; TITLE OF INVENTION: RECEPTOR ASSAY  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065-0900  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/077,675A  
 ; FILING DATE: 3-JUN-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cocuzzo, Anna L.  
 ; REGISTRATION NUMBER: 42,452  
 ; REFERENCE/DOCKET NUMBER: 19590P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 732-594-1273  
 ; TELEFAX: 732-594-4720  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 364 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-077-675A-16

Query Match 31.4%; Score 641; DB 3; Length 364;

Best Local Similarity 45.8%; Pred. No. 2.6e-45;  
Matches 142; Conservative 41; Mismatches 65; Indels 62; Gaps 10;

QY 5 WNGSDGPEGREP-----PWPALPCD---ERRCSPPFLGALVPTAVCLCLFVVGSG 55  
 DB 2 WNAT--PSEEPNVTLDDWDASPGNDSLDELPLFPAPLLAGVTATCVLFFVVGISG 59  
 QY 56 NVVTMLIGRYDMRTTNTNLYLGSMAVSDLLILGLPFDLYLRWRSRPWVFGPLLCRLSL 115  
 DB 60 LLTMLVSRPRELRTTNTNLYLSSMAFSDLLIFLCMLDVLRLMQYRPNNFEGDLCKLPQ 119  
 QY 116 VGECTYATLLHMTALSVERYLAICRPLRARVLTTRRVRALIAVLAVALLSAGPFLF 175  
 DB 120 VFSSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVILVIWAVAFCSAGPIFV 179  
 QY 176 LVGVQDPGISVVGNGTARTASSPLASSPPLMLSRAPPSPPGPETAEEAALFSRECR 235  
 DB 180 LVGVEH-----NGT-----DPRD-----TNEC 197  
 QY 236 RPS--PAQGLARVLMVWTTAYFFLPFLCLSIYLGILGRELMSRRPLRGPAASG---RE 290  
 DB 198 RATEFAVRSGLLTVMVWVSSVFFFLVFCLTVLYSLIGRKLW---RR--RGDAAVGASLRD 253  
 QY 291 RGHQTVRL 300  
 DB 254 QNHQTVKML 263

## RESULT 15

US-09-077-674-16  
 ; Sequence 16, Application US/09077674  
 ; Patent No. 6531314

Search completed: April 11, 2005, 21:06:23  
Job time : 20.8321 secs

Query Match	31.4%;	Score 641;	DB 4;	Length 364;
Best Local Similarity	45.8%;	Pred. No. 2.6e-45;		
Matches 142;	Conservative 41;	Mismatches 65;	Indels 62;	Gaps 10;

  

QY	5	WNGSDGPGAREP-----PWPALPPCD---ERRCSPEPLGALVPVTAACLCFLVVGVS	55
DBb	2	WNAT--PSEEPNPVTTLDLDWDASPGNDSLPDELLPFPAPLAVTATCVAFVVGIS	59
QY	56	NVVTVMILGRYDRMTTNNLYLGSMAVSDLLIILGLPFDLYLRWSRPPWVFGPFLCRLSL	115
DBb	60	NLLTMLVVSRRFELRTTNNLYLSSMAFSDLLIIFLCMPDLDLVRMLQWYRPNWFGDLLCKLFPQ	119
QY	116	YVGECTYATLLHMTALSVERYIAICRPLRARVLVTRRVRALIAVLMAVALLSAGPFLF	175
DBb	120	FVSESTYATVLTITALSVERYFAICPPLRAKVVVTKGRVKVLIVMAVAFCSAGPFI	179
QY	176	LVGVEQDPGISVWVGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSSREC	235
DBb	180	LVGVEHE-----NGT-----DPRD-----TNEC	197
QY	236	RPS--PAQGLRALRYMLWVTTYAFPLPFLCLISLYGLIGRELMSRRRLPFGPAASG---	290
DBb	198	RATEFAVRSGLLTVMVWVSSVFPELPVFCILTVLYSLIGRLKLM--RR--RGDAAVGASLRD	253
QY	291	RGHRTQVRVL	300
DBb	254	QNHKQTQVRL	263

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 11, 2005, 21:05:05 ; Search time 222.023 Seconds  
(without alignments)  
577.198 Million cell updates/sec

Title: US-09-719-485-5

Perfect score: 2043

Sequence: 1 MGSPWNGSDGEGAREPPWP.....WNLHLKHGRFADVLLSVL 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1581	77.4	412	14	US-10-225-567A-473
2	1581	77.4	412	14	US-10-290-078-15
3	1581	77.4	412	14	US-10-318-661-28
4	1581	77.4	412	14	US-10-206-677-2
5	1575	77.1	412	10	US-09-876-252-130
6	1575	77.1	412	15	US-10-417-820A-130
7	1575	77.1	412	15	US-10-417-820A-150
8	1575	77.1	412	16	US-10-723-955-130
9	649	31.8	289	14	US-10-225-567A-140
10	649	31.8	289	14	US-10-303-204A-10
11	643	31.5	366	14	US-10-251-385-88
12	643	31.5	366	14	US-10-303-204A-13
13	641	31.4	289	14	US-10-303-204A-5

14	641	31.4	364	14	US-10-303-204A-16	Sequence 16, Appl
15	639.5	31.3	353	14	US-10-303-204A-3	Sequence 3, Appl
16	639.5	31.3	361	14	US-10-303-204A-8	Sequence 8, Appl
17	637	31.2	366	14	US-10-251-385-210	Sequence 210, App
18	554	27.1	302	14	US-10-303-204A-7	Sequence 7, Appl
19	552	27.0	302	14	US-10-303-204A-2	Sequence 2, Appl
20	454	22.2	271	14	US-10-303-204A-12	Sequence 12, Appl
21	355.5	17.4	445	15	US-10-240-145-53	Sequence 53, Appl
22	355.5	17.4	445	15	US-10-240-145-139	Sequence 139, App
23	354.5	17.4	403	14	US-10-251-385-114	Sequence 114, App
24	354.5	17.4	403	14	US-10-225-567A-540	Sequence 540, App
25	354.5	17.4	403	14	US-10-290-078-18	Sequence 18, Appl
26	354.5	17.4	403	15	US-10-353-690-10	Sequence 10, Appl
27	354.5	17.4	403	16	US-10-915-157-8	Sequence 8, Appl
28	354.5	17.4	422	16	US-10-367-094-141	Sequence 141, App
29	352.5	17.3	403	14	US-10-251-385-224	Sequence 224, App
30	343	16.8	424	16	US-10-915-157-7	Sequence 7, Appl
31	338	16.5	426	15	US-10-311-671-1	Sequence 1, Appl
32	337.5	16.5	293	16	US-10-770-583-12	Sequence 12, Appl
33	337.5	16.5	296	16	US-10-770-583-10	Sequence 10, Appl
34	335	16.4	402	15	US-10-258-423-4	Sequence 4, Appl
35	335	16.4	412	14	US-10-225-567A-557	Sequence 557, App
36	335	16.4	412	16	US-10-770-583-4	Sequence 4, Appl
37	335	16.4	412	16	US-10-770-583-8	Sequence 8, Appl
38	335	16.4	415	10	US-09-875-076-12	Sequence 12, Appl
39	335	16.4	415	10	US-09-876-252-12	Sequence 12, Appl
40	335	16.4	415	14	US-10-272-983-12	Sequence 12, Appl
41	335	16.4	415	14	US-10-393-807-12	Sequence 12, Appl
42	335	16.4	415	15	US-10-358-423-2	Sequence 2, Appl
43	335	16.4	415	15	US-10-417-820A-12	Sequence 12, Appl
44	335	16.4	415	16	US-10-723-955-12	Sequence 12, Appl
45	335	16.4	415	16	US-10-782-596-12	Sequence 12, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-225-567A-473  
; Sequence 473, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225.567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2922  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 473  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-473

Query Match 77.4%; Score 1581; DB 14; Length 412;  
Best Local Similarity 100.0%; Pred. No. 8.9e-117;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSPWNGSDGEGAREPPWPALPCDERRCSPFPGALVPVTAVCLCLFVVGVSQNVTV 60
Db	1	MGSPWNGSDGEGAREPPWPALPCDERRCSPFPGALVPVTAVCLCLFVVGVSQNVTV 60
Qy	61	MLIGRYDMRTTTLNLYLGSMAVSLLILGLPFDLYLWRSPWVFGPLLCRLSLYVGEG 120
Db	61	MLIGRYDMRTTTLNLYLGSMAVSLLILGLPFDLYLWRSPWVFGPLLCRLSLYVGEG 120
Qy	121	CTYATLHMTALSVERYLAIICRLRARVLVTRRRRLIAVLWAVALLSAGPFLVGVG 180

Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGVE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
QY 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300  
Db 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300

RESULT 2  
US-10-290-078-15  
; Sequence 15, Application US/102900078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874  
; FILE REFERENCE: MP12001-288P1(M)  
; CURRENT APPLICATION NUMBER: US/10/290,078  
; CURRENT FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-290-078-15

Query Match 77.4%; Score 1581; DB 14; Length 412;  
Best Local Similarity 100.0%; Pred. No. 8.9e-117; Indels 0; Gaps 0;  
Matches 300; Conservative 0; Mismatches 0

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAIVCLCLFVVGVSNNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAIVCLCLFVVGVSNNVTV 60  
QY 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120  
Db 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120  
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGVE 180  
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGVE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
QY 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300  
Db 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300

RESULT 3  
US-10-318-661-28  
; Sequence 28, Application US/10318661  
; Publication No. US20030167476A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Bruce R.  
; TITLE OF INVENTION: Selective Target Cell Activation By  
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
; TITLE OF INVENTION: Superluciferase  
; FILE REFERENCE: UCAL-049CIP2  
; CURRENT APPLICATION NUMBER: US/10/318,661  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: US 09/341,446  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US97/05334  
; PRIOR FILING DATE: 1997-03-25

; PRIOR APPLICATION NUMBER: US 08/622,348  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-318-661-28

Query Match 77.4%; Score 1581; DB 14; Length 412;  
Best Local Similarity 100.0%; Pred. No. 8.9e-117; Indels 0; Gaps 0;  
Matches 300; Conservative 0; Mismatches 0

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAIVCLCLFVVGVSNNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAIVCLCLFVVGVSNNVTV 60  
QY 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120  
Db 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120  
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGVE 180  
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGVE 180  
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240  
QY 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300  
Db 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300

RESULT 4  
US-10-206-677-2  
; Sequence 2, Application US/10206677  
; Publication No. US20030186336A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences, Inc.  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; APPLICANT: Kullander, Bruce G.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO  
; TITLE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)  
; FILE REFERENCE: 1920-1-8  
; CURRENT APPLICATION NUMBER: US/10/206,677  
; CURRENT FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/250,251  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,452  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-206-677-2

Query Match 77.4%; Score 1581; DB 14; Length 412;  
Best Local Similarity 100.0%; Pred. No. 8.9e-117; Indels 0; Gaps 0;  
Matches 300; Conservative 0; Mismatches 0

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAIVCLCLFVVGVSNNVTV 60  
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAIVCLCLFVVGVSNNVTV 60  
QY 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120  
Db 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPFLCLSLYVGE 120



QY 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVLVGE 180  
DB 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVLVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
QY 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERHRTQVRL 300  
DB 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERHRTQVRL 300

RESULT 5  
US-09-876-252-130  
; Sequence 130, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor  
; FILE REFERENCE: AREN-0054  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/152,524  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/151,114  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/108,029  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; SOFTWARE: Patent in version 3.0  
; NUMBER OF SEQ ID NOS: 146  
; SEQ ID NO 130  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-876-252-130  
Query Match 77.1%; Score 1575; DB 10; Length 412;  
Best Local Similarity 99.7%; Pred. No. 2.7e-116;  
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPPLGALVPVTVAVCLCLFVVGVSNGVTV 60  
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPPLGALVPVTVAVCLCLFVVGVSNGVTV 60  
QY 61 MLIGRYDRMTTNNLYLGSMASVSDLLILLGLPPDLYRLWRSRPWVFGPLCLSLYVGE 120  
DB 61 MLIGRYDRMTTNNLYLGSMASVSDLLILLGLPPDLYRLWRSRPWVFGPLCLSLYVGE 120  
QY 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVLVGE 180  
DB 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVLVGE 180  
QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240  
QY 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERHRTQVRL 300  
DB 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERHRTQVRL 300  
RESULT 6  
US-10-417-820A-130  
; Sequence 130, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled Receptor  
; FILE REFERENCE: 7 US28 CON  
; CURRENT APPLICATION NUMBER: US/10/417,820A  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 130  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-417-820A-130

Query Match 77.1%; Score 1575; DB 15; Length 412;  
Best Local Similarity 99.7%; Pred. No. 2.7e-116;  
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
  
QY 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
DB 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
  
QY 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180  
DB 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180  
  
QY 181 QDPGISVVGNGTARIASSPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240  
DB 181 QDPGISVVGNGTARIASSPPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240  
  
QY 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300  
DB 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 7  
US-10-417-820A-150  
; Sequence 150, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US28.CON  
; CURRENT APPLICATION NUMBER: US/10/417,820A  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 150  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-417-820A-150

Query Match 77.1%; Score 1575; DB 15; Length 412;  
Best Local Similarity 99.7%; Pred. No. 2.7e-116;  
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60  
  
QY 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
DB 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120  
  
QY 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180  
DB 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180  
  
QY 181 QDPGISVVGNGTARIASSPPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240  
DB 181 QDPGISVVGNGTARIASSPPLASSPPLWLSRAPPPSPGPEAAALFSRECRPSA 240  
  
QY 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300  
DB 241 QLGALRVMLWVTYAFYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 8  
US-10-723-955-130  
; Sequence 130, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinsma, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.US29.CON  
; CURRENT APPLICATION NUMBER: US/10/723,955  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 10/417,820  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16





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; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 289
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-5

Query Match      31.4%; Score 641; DB 14; Length 289;
Best Local Similarity 43.3%; Pred. No. 1.3e-42;
Matches 142; Conservative 45; Mismatches 77; Indels 64; Gaps 9;

Qy  5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPPLGALVPVTAACLCIFVVGSGN 56
Db  2 WNATPSEBPGPNLTLPDLGWDAPPENDSLVBELLPLFPPTLLAGVTATCTVALFVVGIG 61
Qy  57 VVTVMILIGYRDMRTTNLYLGSMAVSDLLILGLPFDPDLYRLWRSRPHVFGPLLCRLSLY 116
Db  62 LLTLMVSRFRMRTTNLYLSSMAFSSELLFLCMLPELFLMQYRPNWNLGNLCKUFQF 121
Qy  117 VGEGETATLHMTALSVERYLAICRPLRARVLVTRRRVRLAIVLWAVALLSAGPFLFL 176
Db  122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVILVWAVAFCSAGPIFVL 181
Qy  177 VGVQDQGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTABAAAALFSRRCR 236
Db  182 VGVVHD-----NGT-----DPRD-----TNECR 199
Qy  237 PS--PAQLGALRMLVWTTAYFFLPCLCLSYLGLIGRELSSRRPLRGPASG---RER 291
Db  200 ATEFAVRSGLLTVMVWSSVFFFLPVFCLTVLYSLIGRKLW---RRKRGEAAVGSUKDQ 256
Qy  292 GHRQTVRLKWSRRGSKDACIQSAPPG 319
Db  257 NHKQTVKML-----GGSQCALELSLPG 278

RESULT 14
US-10-303-204A-16
; Sequence 16, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 364
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-3

Query Match      31.3%; Score 639.5; DB 14; Length 353;
Best Local Similarity 47.2%; Pred. No. 2.2e-42;
Matches 137; Conservative 39; Mismatches 61; Indels 53; Gaps 7;

Qy  19 WPALPPCD---ERRCSPPPLGALVPVTAACLCIFVVGSGNVVTVMLIGRYRDMRTTNL 75
Db  8 WDAPPENDSLVBELLPLFPPTLLAGVTATCTVALFVVGIGLNLMLVVRFRMRTTNL 67

; ORGANISM: rattus norvegicus
US-10-303-204A-16

Query Match      31.4%; Score 641; DB 14; Length 364;
Best Local Similarity 45.8%; Pred. No. 1.7e-42;
Matches 142; Conservative 41; Mismatches 65; Indels 62; Gaps 10;

Qy  5 WNGSDGPEGAREP-----PMPALPPCD---ERRCSPPPLGALVPVTAACLCIFVVGSG 55
Db  2 WNAT--PSEEPNVVTLDDMDASFGNDSLDELPLFPAPLLAGVTATCTVALFVVGISG 59
Qy  56 NVTVMLIGRYRDMRTTNLYLGSMAVSDLLILGLPFDPDLYRLWRSRPHVFGPLLCRLSL 115
Db  60 LLTLMVSRFRMRTTNLYLSSMAFSDDLIFCMLPELFLMQYRPNWNGDLCKLUFQ 119
Qy  116 VVGCGCTATLHMTALSVERYLAICRPLRARVLVTRRRVRLAIVLWAVALLSAGPFLF 175
Db  120 FVSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVILVWAVAFCSAGPIFV 179
Qy  176 LVGVEQDQGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTABAAAALFSRRCR 235
Db  180 LVGVEH-----NGT-----DPRD-----TNEC 197
Qy  236 RPS--PAQLGALRMLVWTTAYFFLPCLCLSYLGLIGRELSSRRPLRGPASG---RE 290
Db  198 RATEFAVRSGLLTVMVWSSVFFFLPVFCLTVLYSLIGRKLW---RR--RGDAAVGASLRD 253
Qy  291 RGHROTVRVL 300
Db  254 QNHKQTVKML 263

RESULT 15
US-10-303-204A-3
; Sequence 3, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-3

Query Match      31.3%; Score 639.5; DB 14; Length 353;
Best Local Similarity 47.2%; Pred. No. 2.2e-42;
Matches 137; Conservative 39; Mismatches 61; Indels 53; Gaps 7;

Qy  19 WPALPPCD---ERRCSPPPLGALVPVTAACLCIFVVGSGNVVTVMLIGRYRDMRTTNL 75
Db  8 WDAPPENDSLVBELLPLFPPTLLAGVTATCTVALFVVGIGLNLMLVVRFRMRTTNL 67
```

```
QY 76 YLGSMVSDLLILLGLPFDLYRLMRSPWVGFELLCRLSLYVGECCYATLLHMTALSVE 135
Db 77 YLSSMAFSDLLIFLCMPLDLFRLWQYRPNWLGMLLCKLFQVSESCYATVLTITALSVE 127
QY 136 RYLAICRPLRARVLTTRRRVRALIAVLMAVALLSAGPFLFVGVQDPPGISVVPGLNGTA 195
Db 128 RYFAICFPLRAKVVVTKGRVKLVILVIMAVAFCSAGPIFVLVGVVHD-----NGT- 177
QY 196 RIASSPLASSPPLWLSRAPPPPGPPGPETAEEAALFSRECRPS--PAQLGALRVMLWVTT 253
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVVWVSS 205
QY 254 AYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG---RERGHRTVRVL 300
Db 206 VFFFLFVFCITVLYSLIGRKLW---RRKRGAAVGSLLRDQNHKQIVKWL 252
```

Search completed: April 11, 2005, 21:21:25  
Job time : 223.023 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 11, 2005, 19:24:50 ; Search time 16.4461 Seconds  
(without alignments)  
2258.264 Million cell updates/sec

Title: US-09-719-485-5  
Perfect score: 2043  
Sequence: 1 MGSPWNGSDGPEGAREPPWP.....WQNLHLKHGRFADVDLLSVL 386

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	16.8	424	2 JH0164	neurotensin recept
2	330	16.2	418	2 S29506	neurotensin recept
3	316	15.5	477	2 JC7913	capa receptor (CG1
4	285.5	14.0	418	2 A88013	protein K10B4.4 [i
5	268.5	13.1	416	2 S68822	neurotensin recept
6	261	12.8	595	2 JC8012	G protein-coupled
7	255.5	12.5	378	2 T15816	hypothetical prote
8	253.5	12.4	367	2 JC2421	opioid receptor ho
9	253.5	12.4	367	2 I49022	kappa opioid recep
10	253.5	12.4	367	2 I56520	G protein-coupled
11	253.5	12.4	370	2 S43087	Orphan opioid rece
12	252.5	12.4	658	2 JC8011	G protein-coupled
13	250.5	12.3	363	2 I57940	somatostatin recep
14	249.5	12.2	452	2 JC2459	gastrin/cholecysto
15	249.5	12.2	452	2 A46195	cholecystokinin B
16	248.5	12.2	418	2 A46226	somatostatin recep
17	247	12.1	453	2 S32817	gastrin receptor -
18	245.5	12.0	363	2 I57955	somatostatin recep
19	245.5	12.0	364	2 JN0763	somatostatin recep
20	243	11.9	359	2 JC5277	G protein-coupled
21	241.5	11.8	477	1 QRRUB1	beta-1-adrenergic
22	240	11.7	450	2 JQ1614	gastrin receptor -
23	239	11.7	352	2 JE0296	thyrotropin releas
24	237.5	11.6	447	2 A47430	gastrin/cholecysto
25	237.5	11.6	519	2 S17783	tachykinin recepto
26	234.5	11.5	514	2 D56849	dopamine receptor-
27	233.5	11.4	480	2 I53053	beta 1 adrenergic
28	232.5	11.4	379	2 JC6178	serotonin receptor
29	232.5	11.4	450	2 I49481	alpha-2 adrenergic

30 kappa opioid recep  
31 hypothetical prote  
32 beta-1-adrenergic  
33 gastric CCK-A rece  
34 galanin receptor 2  
35 5-hydroxytryptamin  
36 alpha-2-adrenergic  
37 probable G protein  
38 kappa opioid recep  
39 beta-3-adrenergic  
40 thyrotropin-releas  
41 cholecystokinin re  
42 thyrotropin-relea  
43 thyroliberin recep  
44 somatostatin recep  
45 beta-adrenergic re

232 11.4 380 2 A55259  
230 11.3 477 2 T25846  
229.5 11.2 466 2 S36794  
229 11.2 427 2 S50150  
228.5 11.2 387 2 JC5949  
228 11.2 437 2 I57942  
228 11.2 450 2 B40392  
227.5 11.1 428 2 S30508  
227 11.1 380 2 JC2338  
227 11.1 418 2 G02953  
226 11.1 398 2 JN0708  
225 11.0 444 2 A42685  
224.5 11.0 411 2 I56444  
224.5 11.0 412 2 S23436  
224.5 11.0 428 2 A44021  
224 11.0 483 2 A25896

## ALIGNMENTS

### RESULT 1

JH0164  
neurotensin receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C:Accession: JH0164  
R:Tanaka, K.; Masu, M.; Nakanishi, S.  
Neuron 4, 847-854, 1990  
A:Title: Structure and functional expression of the cloned rat neurotensin receptor.  
A:Reference number: JH0164; MUID:90297956; PMID:1694443  
A:Accession: JH0164  
A:Molecule type: mRNA  
A:Residues: 1-424 <TAN>  
A:Cross-references: UNIPROT:P20789  
C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. The  
ter (neuromodulator in the brain and as a hormone) cellular mediator in peripheral tiss  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:65-87/Domain: transmembrane #status predicted <TM1>  
F:97-121/Domain: transmembrane #status predicted <TM2>  
F:144-165/Domain: transmembrane #status predicted <TM3>  
F:189-210/Domain: transmembrane #status predicted <TM4>  
F:236-260/Domain: transmembrane #status predicted <TM5>  
F:309-330/Domain: transmembrane #status predicted <TM6>  
F:348-372/Domain: transmembrane #status predicted <TM7>  
F:4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.8%; Score 343; DB 2; Length 424;  
Best Local Similarity 33.9%; Pred. NO. 9.3e-19;  
Matches 82; Conservative 41; Mismatches 71; Indels 48; Gaps 6;

QY 39 VPVTAVCLCLFVGVGSGNVVTVMLIGR---YRDMRTTNLVIGSMVSDLLI-LGLPFD 94  
DB 65 VLVTAIYALFVGVGVGNSVTAFTLARKKSIQSLQSTVHYHLGSLSDLLILLAMPVE 124  
QY 95 LYR-LWRSRPVVFGLLCRLSLYVGEGETYATLHMTALSVERYLAI CRFLARVLVTRR 153  
DB 125 LYNFIWVHPWAFGDAGCGYFFLEDACTATALNVASLSVERYLAI CHPPKAKTLMRSR 184  
QY 154 RVRALIAVLWAVALLSAGPFPLFLVGVEQDPGISVVVPLNGTARIASSPLASSPPLWLSRA 213  
DB 185 RTKKFPISAIWLASALLAIPMLFTMGLQNRSGDTHPG-----GLVCTPIVDT----- 231  
QY 214 PPPPPSPGPTAEAAALFSPRCRSPAQGLGALRVMLWTTAYFFL-PELCILSYGLIGR 272  
DB 232 -----ATVKVVIQVNTFMSFLFPMLVISILNTVIAN 262  
QY 273 EL 274  
DB 263 KL 264





A:Reference number: S68822; MUID:96228041; PMID:8647296

A:Accession: S68822

A:Molecule type: mRNA

A:Residues: 1-416 <CHA>

A:Cross-references: UNIPROT:Q63384; GB:X97121; NID:g1483579; PIDN:CAA65787.1; PID:g14835

A:Experimental source: hypothalamus

A:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:33-58/Domain: transmembrane #status predicted <TM1>

F:70-91/Domain: transmembrane #status predicted <TM2>

F:110-131/Domain: transmembrane #status predicted <TM3>

F:155-175/Domain: transmembrane #status predicted <TM4>

F:204-230/Domain: transmembrane #status predicted <TM5>

F:296-315/Domain: transmembrane #status predicted <TM6>

F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 13.1%; Score 268.5; DB 2; Length 416;

Best Local Similarity 37.9%; Pred. No. 4.3e-13;

Matches 66; Conservative 33; Mismatches 66; Indels 9; Gaps 4;

Qy 18 PWPALP-----PCDERCSPPLGALVPVAVCLCFVVGSGNVVMTLIGRYDMRT 71

Db 6 PWPPRPSPSAGLSLEARLGVDTLWAKVLTALYSLIFAFGTAGNALSVHVLKARAGR 65

Qy 72 -TTNLYLGMAVSDLLILL-GLPDLR-LWRSRPWVGPGLCRSLYVGGCTYATLLH 128

Db 66 GLRHYVLSLALSALLLVMPMELYNFVWVSHYPVWFGDLGCRGYFVRELCAATVLS 125

Qy 129 MTALSVERYLAICRPLRVLVTRRRVALLAVALLSAGPLFLVGVQED 182

Db 126 VASLSAEKCLAVCQLRRLRLTRRLSLVWASGLPALPWAIVMGKHE 179

RESULT 6

JC8012

C:Protein-coupled neuropeptide pyrokinin-2 receptor (CG8795) - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 04-Apr-2004 #sequence\_revision 04-Apr-2004 #text\_change 04-Apr-2004

C:Accession: JC8012

R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R.

Biochem. Biophys. Res. Commun. 309, 485-494, 2003

A:Title: Molecular cloning, functional expression, and gene silencing of two *Drosophila*

A:Reference number: JC8011; PMID: 12951076

A:Accession: JC8012

A:Molecule type: mRNA

A:Residues: 1-595 <ROS>

A:Cross-references: GB:AV277899

C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as

e, feeding, and behavior.

C:Genetics:

A:Gene: CG8795

A:Introns: 115/1; 170/2; 214/3; 281/1; 352/3; 390/3

C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 12.8%; Score 261; DB 2; Length 595;

Best Local Similarity 29.7%; Pred. No. 2.3e-12;

Matches 78; Conservative 37; Mismatches 104; Indels 44; Gaps 8;

Qy 34 PLGLVPTAVTAVCLCFVVGSGNVVMTLIGRYDMRTTNLYLGMAVSDLLILL-CLP 92

Db 58 PLSLIATLUSGVALIFAGVLGNLTICIVSRNFMHTATNPFYLFNLAISDMILICSGMP 117

Qy 93 FDLRLMRSRPWVGPGLCRSLYVGGCTYATLHMTALSVERYLAICRPLRVLVTR 152

Db 118 QDLNLMHPDNPYPSDSICILESVLSEANATVLTITAFVVERVIALCHPFRQHTMSKL 177

Qy 153 RVRRLIAVLWALLSAGPLFLVGVQEDPGISVVGINGVARIASS-----PLASSPPL 208

Db 178 SRAVKFIFAIWTAALLALPOAIPQSV-----VWQMGTSCTMKNDFFAFVAVSGFL 230

Qy 209 WLSRAPSPSPSGPETA-----EAAALFSREC-----RSPALGALRWML 249

Db 231 FF-----GGPMTAICVLYVLGVKLRSLRLQALPRRCYDVMRGISAQTRVIRMLV 281

Qy 250 WVTYAYF--FLPFLC--LSILYG 268

Db 282 AVAVAFICWAPFHAQRLMAVYG 304

RESULT 7

TI5816

hypothetical protein C48C5.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: TI5816

R:Pavello, A.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of *C. elegans* cosmid C48C5.

A:Reference number: Z18410

A:Accession: TI5816

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-378 <FAV>

A:Cross-references: UNIPROT:Q18701; EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB370

A:Experimental source: strain Bristol N2; clone C48C5

C:Genetics:

A:Gene: CESP-C48C5.1

A:Map position: X

A:Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1

C:Superfamily: adenosine receptor A1

Query Match 12.5%; Score 255.5; DB 2; Length 378;

Best Local Similarity 27.0%; Pred. No. 3.9e-12;

Matches 66; Conservative 49; Mismatches 96; Indels 33; Gaps 6;

Qy 38 LVPVAVCLCLFVVGSGNVVMTLIGRYDMRTTNLYLGMAVSDLLILL-LGLPFDLY 96

Db 51 LYKVTALYIFLFGVIGNTTCLVMKHPMKTHASWYLMNLAVSDLVTLVGLPFEVM 110

Qy 97 RLWRSRPWVGPGLCRSLYVGGCTYATLHMTALSVERYLAICRPL-RARVLVTRRV 155

Db 111 MNWQYWPMPDYICNLKALIAETTSVSILTIFAERYVAVCHPLFLMKVQPFKNI 170

Qy 156 RALLAVLWALLSAGPLFLVGVQEDPGISVVGINGVARIASSPLASSPLMLSRAPP 215

Db 171 GTIIGTWIFSILCAMP--FAIHRADYIMKSWGTDNRIPVKSXKMCN----- 217

Qy 216 PSPSPGPETAFAALFSGRECRPSPAQLGALRWML-WVTYAYFFLPFLCLSLYGLIGREL 274

Db 218 -----IAYMF-----EPKLASTFKILFHFSIAIAFFALPLFTVILYARIACKV 260

Qy 275 WSSR'278

Db 261 SSNR 264

RESULT 8

JC2421

opioid receptor homolog, MOR-C - mouse

C:Species: *Mus musculus* (house mouse)

C:Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004

C:Accession: JC2421; I49122

R:Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.

Biochem. Biophys. Res. Commun. 205, 1353-1357, 1994

A:Title: Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor

A:Reference number: JC2434; MUID:95100967; PMID:7802669

A:Accession: JC2421

A:Molecule type: mRNA

A:Residues: 1-367 <NTS>

A:Cross-references: UNIPROT:P35377; DBJ:D31663

R:Halford, W.P.; Gebhardt, B.M.; Carr, D.J.

J. Neuroimmunol. 59, 91-101, 1995

A:Title: Functional role and sequence analysis of a lymphocyte orphan opioid receptor.

A:Reference number: I49122; MUID:95318231; PMID:7797625

A:Accession: I49122

A:Status: preliminary; translated from GB/EMBL/DBJ



```
Db 44 PLGLKVTIVGLYLAIVCIGLLGNCLVMYVILRHTKMTATNIYIFNLALADTLVLLTLPF 103
Qy 94 ---DLYRLWRSRPWVFGPLLCRLSLYVGEGETYATLLHMTALSVERYLAICRPLRARVLV 150
Db 104 QGTDLILGF----WFGNALCKTVIAIDYNNMFTSTFTLTAMSDVRYVAICHPIRALDVR 159
Qy 151 TRRRVRALIAVLWAVALLSAGPFLVGVGQDPGIVVPGVGLNGTARIASSPPLASPPPLWL 210
Db 160 TSSKAQAVNVAIWALASV-----VGVPVAIMGSAQVDEBIEC-----L 198
Qy 211 SRAPPPSPSGPETAEEAALFSRECRPSPAQLGALRVMLWVTAVFFLPFLCLSLYGLI 270
Db 199 VEIPAPQDYWGVPFAICIFLES-----FIIPVLISVCYSLSM 235
Qy 271 GRELWSSRRPLRGPAASGRGRHQTQTVRLR 301
Db 236 IRLRGVR-----LLSGSREKDRNLRI 260

RESULT 11
S43087
orphan opioid receptor ORL1 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43087; G01892
R:Moillerieu, C.; Parmentier, M.; Mailleux, P.; Butour, J.L.; Moissand, C.; Chalon, P.; Ca
FEBS Lett. 341, 33-38, 1994
A:Title: ORL1, a novel member of the opioid receptor family. Cloning, functional expres
A:Reference number: S43087; MUID:94185768; PMID:8137918
A:Accession: S43087
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-370 <MOL>
A:Cross-references: UNIPROT:P41146; EMBL:X77130; NID:G471316; PIDN:CAA54386.1; PID:G4713
R:Lee P., H
submitted to the EMBL Data Library, June 1995
A:Reference number: H00703
A:Accession: G01892
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-370 <LEES>
A:Cross-references: EMBL:U30185; NID:g1144296; PIDN:AAA84913.1; PID:g1144297
C:Genetics:
A:Gene: GDB:OPRL1
A:Cross-references: GDB:345029
A:Map position: 8q11.2-8q11.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.4%; Score 253.5; DB 2; Length 370;
Best Local Similarity 26.9%; Pred. No. 5.4e-12;
Matches 73; Conservative 46; Mismatches 95; Indels 57; Gaps 6;

Qy 34 PLGLAPVTAVCLCLFVGVGSGNVVTVMLIGRYDRMTTNNLYGSMVAVSLLILLGLPFP 93
Db 47 PLGLKVTIVGLYLAIVCIGLLGNCLVMYVILRHTKMTATNIYIFNLALADTLVLLTLPF 106
Qy 94 ---DLYRLWRSRPWVFGPLLCRLSLYVGEGETYATLLHMTALSVERYLAICRPLRARVLV 150
Db 107 QGTDLILGF----WFGNALCKTVIAIDYNNMFTSTFTLTAMSDVRYVAICHPIRALDVR 162
Qy 151 TRRRVRALIAVLWAVALLSAGPFLVGVGQDPGIVVPGVGLNGTARIASSPPLASPPPLWL 210
Db 163 TSSKAQAVNVAIWALASV-----VGVPVAIMGSAQVDEBIEC-----L 201
Qy 211 SRAPPPSPSGPETAEEAALFSRECRPSPAQLGALRVMLWVTAVFFLPFLCLSLYGLI 270
Db 202 VEIPTPDQYWGVPFAICIFLES-----FIVPVLISVCYSLSM 238
Qy 271 GRELWSSRRPLRGPAASGRGRHQTQTVRLR 301
Db 239 IRLRGVR-----LLSGSREKDRNLRI 263
```

## RESULT 12

```
JC8011
G protein-coupled neuropeptide pyrokinin-2 receptor (CG8784) - fruit fly (Drosophila mel
C:Species: Drosophila melanogaster
C>Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: JC8011
R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: JC8011; PMID: 12951076
A:Accession: JC8011
A:Molecule type: mRNA
A:Residues: 1-658 <ROS>
A:Cross-references: GB:AY277898
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
evolution, diapause, feeding, and behavior.
C:Genetics:
A:Gene: CG8784
A:Introns: 160/1; 215/2; 259/3; 326/1; 400/3
C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 12.4%; Score 252.5; DB 2; Length 658;
Best Local Similarity 30.8%; Pred. No. 1.1e-11;
Matches 92; Conservative 43; Mismatches 103; Indels 61; Gaps 14;

Qy 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLC---LPVVGVSGNV 57
Db 83 LGST-NGTNASTMAAD-----SPVDE-----SLTETALTVCYALFVAGVGLNL 126
Qy 58 VTVMILIGRYDRMTTNNLYGSMVAVSLLILL-GLPFDLYRLWRSRPWVFGPLLCRLSLY 116
Db 127 ITCVISRNNPMHTATNPFYFNLAVALSDILLVSGIQELYNLWYPMYPFTDAMCMGVS 186
Qy 117 VGECTATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIALVLAVALISAGP--FL 174
Db 187 LSEMAANATVITITFTVRYIAICHPROHTMSKLSRAIKFIFAIWLAFLALPQAMQ 246
Qy 175 FLVGVGQDPGIVVPGVGLNGTARIASSPPLASPPPLWLSRAPPPSPGPETAEEAALF--- 231
Db 247 FSV-VYQNEGVSCTMENDFYAHV----FAVSGPIFF-----GGPMTA-ICVLYVLI 291
Qy 232 -----GRECPSP-----AQGLARVLMVWVTAYF--FLPFLC--LSLYGL 269
Db 292 GVKLKRSLQLSPRTFDANRGLNAQGRVIRMLVAVAFELCWAPPHQAQLMAVYGL 350

RESULT 13
157940
somatostatin receptor 5 - rat
N:Alternate names: somatotropin release-inhibiting factor subtype 28 receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: 157940; 157949; S39244
R:O'Carroll, A.M.; Lolait, S.J.; Koni, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939-946, 1992
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A:Reference number: 157940; MUID:93125499; PMID:1362243
A:Accession: 157940
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-363 <OCAL>
A:Cross-references: UNIPROT:P0938; GB:L04535; NID:G409238; PIDN:AAA17029.1; PID:G409239
R:O'Carroll, A.M.; Lolait, S.J.; Koni, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A:Reference number: 157949; MUID:94088493; PMID:8264565
A:Accession: 157949
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 341-363 <OCA2>
A:Cross-references: GB:S67370; NID:G455947; PIDN:AAB29371.1; PID:G455948
A:Experimental source: pituitary
```

R; Penetta, R.; Greenwood, M.; Patel, Y.C.  
submitted to the EMBL Data Library, August 1993  
A; Description: Correction of the nucleotide and amino acid sequence of the rat somatostatin-like peptide.  
A; Reference number: S39244  
A; Accession: S39244  
A; Molecule type: mRNA  
A; Residues: 309-363 <PEN>  
A; Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912  
C; Geneticks:  
A; Gene: SSIR5  
C; Superfamily: vertebrate rhodopsin

Query Match	12.3%	Score 250.5;	DB 2;	Length 363;
Best Local Similarity	26.7%;	Pred. No. 8.9e-12;		
Matches	76; Conservative	43; Mismatches	99; Indels	67; Gaps 8

Qy	5	WNGSGPGEGAREPPMPALPPCDERRCCSFPLGA---	LVPVTA	VC	LC	LV	VG	SG	NV	VT	VM	61	
Db	12	NNASAASGNHN--WSLVG-----	SASPMGAR	VL	VP	VL	YLLV	C--	TV	GL	SG	NTLV	60
Qy	62	LIGRYDRMTTNLYLGSMAVSDLLIILGLPFDLYRLWRSRPWVFP	LC	RL	CR	LS	LV	YG	GC			121	
Db	61	VYERAKKKTVTNTVILNLAVADVFLMGLPFLATQNAVVSYPFGS	FL	CR	LV	MT	LD	GIN				120	
Qy	122	TYATLHMTALSVERYLAICRPLRRLVLTTRRRVRLIALVLM	VA	LL	AG	PF	LV	GEQ				181	
Db	121	QFTSIFCLMWSVDYLAIVHPLFSARWRPRVAKWASA	AV	VS	LL	MS	LP	LV	AD	VQE		180	
Qy	182	DGSIWVPLGNGTARIASSPLASSPPIWLSRAPPPSPG	PT	AA	LF	SR	CP	SP	QAQ			241	
Db	181	G-----WGTCNLS-----w-----	PE	VG								194	

Qy 242 LGALRVMLVWVTTAVFFLPFLCLSLVGLI-----GRELWSSRR 279  
Db 195 LWCAAFITVTSVLGFFGGLPVICLCVLLI VVKVAAGRWVGSSRR 239

RESULT 14  
JC2459 gastrin/cholecystokinin B receptor - rabbit  
JC2459 C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
C:Accession: JC2459  
R:Blandizzi, C.; Song, I.; Yamada, T.  
Biochem. Biophys. Res. Commun. 202, 947-953, 1994  
A>Title: Molecular cloning and structural analysis of the rabbit gastrin/CCRB receptor  
A:Reference number: JC2459; MUID:94324990; PMID:8048969

A:Accession: J02459  
 A:Molecule type: mRNA  
 A:Residues: 1-452 <BLA>  
 A:Cross-references: UNIPROT:P46627; GB:L31548; NID:G495663; PIDN:AAA31194.1; PID:G495665  
 C:Genetics:  
 A:Introns: 49/1; 133/1; 216/2; 273/1  
 C:Superfamily: neurokinin 1 receptor  
 C:Keywords: receptor; transmembrane protein  
 F:56-79/Domain: transmembrane #status predicted <TM1>  
 F:85-104/Domain: transmembrane #status predicted <TM2>  
 F:130-149/Domain: transmembrane #status predicted <TM3>  
 F:169-187/Domain: transmembrane #status predicted <TM4>  
 F:217-237/Domain: transmembrane #status predicted <TM5>  
 F:339-359/Domain: transmembrane #status predicted <TM6>  
 F:381-400/Domain: transmembrane #status predicted <TM7>

Query Match	12.2%	Score 249.5	DB 2	Length 452
Best Local Similarity	25.2%	Pred. No. 1.3e-11		
Matches 86	Conservative	50	Mismatches 122	Indels 83
				Gaps 10

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48 LFVGVGNVTVMLIGRYEDMETNTNLYLGSNAVSDLLILG-LPFDLYLWRSRP--- 103
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
62 IFLMSGVGNILIIIVLGLSRRLRTVTNAFLSLAVSDLLILAVACMPFTLL-----PNLM 115
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
104 --WTFGPLLCLSLSYVCGECTYATLHMTALSVRYLAI CRPLRLARVLVTRRRVRAIIAV 161
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

Search completed: April 11, 2005, 21:05:37  
Job time : 18.4461 secs

Db	116	GTTFIEGTICKAVSYLMGVSVSTLSLVAITALERYSAICRPLQARVMQTRGHAARVILA	175
Qy	162	LMAVALLSAGPFLFLVGEQDPGISVVPCLNGTARIASSPLASSPPLMLSRAPPPSPSG	221
Db	176	TWLSGLLMVPYPVYTAQ-----	197
Qy	222	PETABAAALFGRCPSPQAQALXRVMLWVTYFFLPFLCLSLYGLIGRELWSRR--	279
Db	198	PRVLQCVHRW-----PSARVQRTWSVLKLL--LUFFVPGVMAVAYGLISRELYLGLRFD	250
Qy	280	-----PLRGPAAAGRGRHQTQTVLRKWSRRGSK-DACLOSAPGTAQT	323
Db	251	SDSDSESOSRVRGQGLPGGAAPGV--HNGRCRPEAGLAGEDGDCYQVLPNSR---	304
Qy	324	LGPIPLLAQLWAPIAPPFISIPASTRRGGSGIYNLIVAL	364
Db	305	--PALESALTAPISGGPGFPRQAQAKLAKKRVVRLMVI	343

RESULT 15

A46195  
cholecystokinin B receptor subtype - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A46195  
R:Wank, S.A.; Pisegna, J.R.; de Weerth, A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8691-8695, 1992  
A:Title: Brain and gastrointestinal cholecystokinin receptor family: structure and function  
A:Reference number: A46195; MUID:92409582; PMID:1528881  
A:Accession: A46195  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-452 <WAN>  
A:Cross-references: UNIPROT:P30553; GB:M99418; NID:G203459; PIDN:AAA40925.1; PID:G203460  
A:Experimental source: brain  
A:Note: sequence extracted from NCBI backbone (NCBI:114083, NCBI:P114084)  
C:Superfamily: neurokinin 1 receptor  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	12.2%	Score	249.5;	DB 2;	Length	452;	
Best Local Similarity	26.1%	Pred. No.	1.3e-11;				
Matches	84;	Conservative	51;	Mismatches	96;		
				Indels	91;	Gaps	13;

[illegible]

Search completed: April 11, 2005, 21:05:37  
Job time : 18.4461 secs